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OM nucleic - nucleic search, using sw model

Run on: October 22, 2003, 05:06:29 ; Search time 81 seconds

(without alignments)
4086.881 Million cell updates/sec

Title: US-09-978-273-2

Perfect score: 750

Sequence: 1 atgaaagaatagtgccaaa.....ctactgcgctgctaataa 750

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/6C COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	740.8	98.8	847	1	US-08-378-761A-20
2	740.8	98.8	847	1	US-08-485-286-20
3	740.8	98.8	978	1	US-08-378-761A-10
4	740.8	98.8	978	1	US-08-485-286-10
5	740.8	98.8	985	1	US-08-378-761A-8
6	740.8	98.8	985	1	US-08-485-286-8
7	740.8	98.8	1161	1	US-08-378-761A-14
8	740.8	98.8	1161	1	US-08-485-286-14
9	740.8	98.8	1422	1	US-08-378-761A-16
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11	740.8	98.8	1683	1	US-08-378-761A-18
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13	740.8	98.8	1695	1	US-08-378-761A-22
14	740.8	98.8	1695	1	US-08-485-286-22
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17	737.8	98.4	1029	6	5248606-40
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19	737.8	98.4	1029	1	US-08-485-286-6
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22	718.8	95.8	987	6	5248606-42
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24	655.8	87.4	1074	1	US-08-378-761A-4
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27	652.8	87.0	1076	1	US-08-378-761A-1

28	652.8	87.0	1076	1	US-08-485-286-1	Sequence 1, Appli
29	652.8	87.0	1105	1	US-08-378-761A-3	Sequence 3, Appli
30	652.8	87.0	1105	1	US-08-485-286-3	Sequence 3, Appli
31	652.8	87.0	1105	6	5248606-39	Patent No. 5248606
32	652.6	87.0	1053	3	US-09-097-767A-13	Sequence 13, Appli
33	651.2	86.8	1076	6	5248606-1	Patent No. 5248606
34	649.8	86.6	944	3	US-09-097-767A-16	Sequence 16, Appli
35	649.8	86.6	1244	3	US-09-097-767A-22	Sequence 22, Appli
36	636.8	84.9	1245	3	US-09-097-767A-25	Sequence 25, Appli
37	510.8	68.1	1934	1	US-07-941-651-1	Sequence 1, Appli
38	510.8	68.1	1934	1	US-08-279-996-1	Sequence 1, Appli
39	308	41.1	533	3	US-09-097-767A-36	Sequence 36, Appli
40	93	12.4	93	1	US-08-378-761A-39	Sequence 39, Appli
41	93	12.4	93	1	US-08-485-286-39	Sequence 39, Appli
42	77.6	10.3	846	1	US-07-901-707-12	Sequence 12, Appli
43	77.6	10.3	846	1	US-07-988-430-12	Sequence 12, Appli
44	77.6	10.3	846	1	US-08-425-336-12	Sequence 12, Appli
45	77.6	10.3	846	1	US-08-488-113B-12	Sequence 12, Appli

ALIGNMENTS

RESULT 1
US-08-378-761A-20
; Sequence 20, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,761A
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 847 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 51...845
US-08-378-761A-20

Query Match 98.8%; Score 740.8; DB 1; Length 847;
Best Local Similarity 99.7%; Pred. No. 3.2e-152;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGAAAGAAATAGTGCACAAAGTTCAATCTTCCCGTGAGGACGCGAAGTACCT 60

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Db 111 ATGAAAGATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGACGCGAACTACCT 110
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Db 111 TACAGCCCTTTATCGGCTCGGTCCGGAAGACGTGATCAAACTGACACGACCATATAA 170
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Db 171 GGGATCTTCAGCCCGTGTGCTCCACCGGAGAAAGTCCGAGCTATGTTCTACACA 230
Qy 181 GAATCTGAAACTAGACAGCTCCATCACCTGCCATGCGATGCGATGCGATGCGATGCG 240
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Db 411 AACAAGGCTCTGAGACCGCTCACCATGGCGCGCGGATGACCAAGGACGCGACAC 470
Qy 421 CTGGCAAGAAAGAGGCGGTGACCTTCAAGGACGCGACACCAAGGACGCGACAC 480
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Qy 481 CTGGTGTCTATGCTGCTGAGGCGGTGCGGTTCACACCGTGTCCGCGACGCGAC 540
Db 531 CTGGTGTCTATGCTGCTGAGGCGGTGCGGTTCACACCGTGTCCGCGACGCGAC 590
Qy 541 GGGTTCAACAGCAGCAGCGGCTGACCTTGAGCGGCGGAGGAGGAGGAGGAGGAG 600
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Qy 601 TGGGACAGGATCTCCAAAGCGGCGCTTCGAGTGGGCTGACCAACCCACCGCTGTGATCCC 660

RESULT 2
US-08-485-286-20
; Sequence 20, Application US/08485286
; Patent No. 5646026
; Patent No. 5646026 5646119
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,286
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: US 08/378761
; APPLICATION NUMBER:
; FILING DATE: 26-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 847 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 51..845
; US-08-485-286-20

Query Match 98.8%; Score 740.8; DB 1; Length 847;
Best Local Similarity 99.7%; Pred. No. 3.2e-152;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 51 ATGAAAGATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGACGCGAACTACCT 110
Qy 61 TACAGCCCTTTATCGGCTCGGTCCGGAAGACGTGATCAAACTGACACGACCATATAA 120
Db 111 TACAGCCCTTTATCGGCTCGGTCCGGAAGACGTGATCAAACTGACACGACCATATAA 170
Qy 121 GGGATCTTCAGCCCGTGTGCTCCACCGGAGAAAGTCCGAGCTATGTTCTACACA 180
Db 171 GGGATCTTCAGCCCGTGTGCTCCACCGGAGAAAGTCCGAGCTATGTTCTACACA 230
Qy 181 GAATCTGAAACTAGACAGCTCCATCACCTGCCATGCGATGCGATGCGATGCGATGCG 240
Db 231 GAGCTCAAACTAGACAGCTCCATCACCTGCCATGCGATGCGATGCGATGCGATGCG 290
Qy 241 GTGGCTTCAGGACCCCGGGGCTGTGCTGGAGTTCGGCAAGGACGCGACACCCAC 300
Db 291 GTGGCTTCAGGACCCCGGGGCTGTGCTGGAGTTCGGCAAGGACGCGACACCCAC 350
Qy 301 CTCTCGGCGACACCCCGGCTGTGCTGGAGTTCGGCAAGGACGCGACACCCAC 360
Db 351 CTCTCGGCGACACCCCGGCTGTGCTGGAGTTCGGCAAGGACGCGACACCCAC 410
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Db 411 AACAAGGCTCTGAGACCGCTCACCATGGCGCGCGGATGACCAAGGACGCGACAC 470
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Db 471 CTGGCAAGAAAGAGGCGGTGACCTTCAAGGACGCGACACCAAGGACGCGACAC 530
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Db 531 CTGGTGTCTATGCTGCTGAGGCGGTGCGGTTCACACCGTGTCCGCGACGCGAC 590
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Db 591 GGGTTCAACAGCAGCAGCGGCTGACCTTGAGCGGCGGAGGAGGAGGAGGAGGAG 650
Qy 601 TGGGACAGGATCTCCAAAGCGGCGCTTCGAGTGGGCTGACCAACCCACCGCTGTGATCCC 660
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Db 651 TGGGACAGGATCTCCAAAGCGGCTTCGAGTGGGCTGACCAACCCACCGCTGTGATCCCC 710
QY 661 GACATCAGAAGCTTCGSCATCAAGGATAAGAAAGCAAGCAGGAGGATCGTTGCGCTCGTT 720
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QY 721 AAGAATCAAACTACTGCCGCTGCC 744
Db 771 AAGAATCAAACTACTGCCGCTGCC 794

RESULT 3
US-08-378-761A-10
; Sequence 10, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 978 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 51..815
US-08-378-761A-10

Query Match 98.8%; Score 740.8; DB 1; Length 978;
Best Local Similarity 99.7%; Pred. No. 3.3e-152;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAAGAATAGTGCAAGTTTCATGAAATCTCCCGTGGAGACGCGAACTACCT 60
Db 51 ATGAAAGAATAGTGCAAGTTTCATGAAATCTCCCGTGGAGACGCGAACTACCT 110
QY 61 TACAGCGCTTCATCGCTCGGTCGCGAAGACGTGATCAAACTGCAACGACGATAAA 120
Db 111 TACAGCGCTTCATCGCTCGGTCGCGAAGACGTGATCAAACTGCAACGACGATAAA 170
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QY 361 AACAGGGTCTCGAGACCCGCTCAACATGGGCCCGCGCGAAATGACAGGGCGCTCAACGAC 420
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Db 531 CTGGTGTTCATGTTGCGAGGGGCTGCGGTTCAACACCGTGTCCGCGACGCTGGACGCG 590
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Db 651 TGGGACAGATCTCAAAGCGCGCTTCGAGTGGGCTGACCAACCGCTGTGATCCCC 710
QY 661 GACATGCAAGCTTGGCATCAAGGATAAGAAAGCAAGCAGGAGGATCGTTGCGCTCGTT 720
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QY 721 AAGAATCAAACTACTGCCGCTGCC 744
Db 771 AAGAATCAAACTACTGCCGCTGCC 794

RESULT 4
US-08-485-286-10
; Sequence 10, Application US/08485286
; Patent No. 5646026
; Patent No. 5646026 5646119
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,286
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/378761
; FILING DATE: 26-JAN-1995

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Db AACAGGCTCTGGAGACCGTCAACATGGCGCGCCGAAATGACAGGCGCGTCAACGAC 456
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Db CTGTGTGTCTATGTTGTCGAGGGGCTCGGTTCAACACCGTTCACCGACGGTGGACGCG 576
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601 TGGGACAGGATCTCCAGGCGGCTTCGAGTGGGCTGACACCCGCTGTGATCCCC 660
Db TGGGACAGGATCTCCAGGCGGCTTCGAGTGGGCTGACACCCGCTGTGATCCCC 696
661 GACATGACAGAGCTTGGCATCAAGGATAAGAAAGAGAGAGAGAGCTGGTGGCTCGTT 720
Db GACATGACAGAGCTTGGCATCAAGGATAAGAAAGAGAGAGAGAGCTGGTGGCTCGTT 756
721 AAGATCAAACTACTGCGGCTGCC 744
Db AAGATCAAACTACTGCGGCTGCC 780

RESULT 6

US-08-485-286-8
; Sequence 8, Application US/08485286
; Patent No. 5646026
; Patent No. 5646026 5646119
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,286
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/378761
; FILING DATE: 26-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 985 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 37..822
US-08-485-286-8

Query Match 98.8%; Score 740.8; DB 1; Length 985;
Best Local Similarity 99.7%; Pred. No. 3.3e-152;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGAAAGAATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGGACGCGAACTACCT 60
Db 37 ATGAAAGAATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGGACGCGAACTACCT 96
Qy 61 TACAGCGCTTCATCGGTCGGTCCGGAAGAGCTGATCAAACTGCACCGACCAATAA 120
Db 97 TACAGCGCTTCATCGGTCGGTCCGGAAGAGCTGATCAAACTGCACCGACCAATAA 156
Qy 121 GGGATCTTCCAGCCCGTGTGCTGCCACCGGAGAGAGGTCGCCGAGCTATGTTCTACACA 180
Db 157 GGGATCTTCCAGCCCGTGTGCTGCCACCGGAGAGAGAGGTCGCCGAGCTATGTTCTACACA 216
Qy 181 GAATGAAATCTAGACAGCTCCATCAAGCTGCCATAGCATGGAACCTGTACCTC 240
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Db 697 GACATGACAGAGCTTGGCATCAAGGATAAGAAAGAGAGAGAGAGCTGTGCGCTCGTT 756
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Db 757 AAGATCAAACTACTGCGGCTGCC 780

RESULT 7

US-08-378-761A-14
; Sequence 14, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF

/	TITLE OF INVENTION:	USING
/	NUMBER OF SEQUENCES:	81
/	CORRESPONDENCE ADDRESS:	
/	ADDRESSEE:	ANDREA T. BORUCKI
/	STREET:	9330 ZIONSVILLE ROAD
/	CITY:	INDIANAPOLIS
/	STATE:	IN
/	COUNTRY:	US
/	ZIP:	46268
/	COMPUTER READABLE FORM:	
/	MEDIUM TYPE:	Floppy disk
/	COMPUTER:	IBM PC compatible
/	OPERATING SYSTEM:	PC-DOS/MS-DOS
/	SOFTWARE:	PatentIn Release #1.0, Version #1.25
/	CURRENT APPLICATION DATA:	
/	APPLICATION NUMBER:	US/08/378,761A
/	FILING DATE:	26-JAN-1995
/	CLASSIFICATION:	435
/	ATTORNEY/AGENT INFORMATION:	
/	NAME:	BORUCKI, ANDREA T
/	REGISTRATION NUMBER:	33651
/	REFERENCE/DOCKET NUMBER:	38272B
/	TELECOMMUNICATION INFORMATION:	
/	TELEPHONE:	(317) 337-4846
/	INFORMATION FOR SEQ ID NO:	14:
/	SEQUENCE CHARACTERISTICS:	
/	LENGTH:	1161 base pairs
/	TYPE:	nucleic acid
/	STRANDEDNESS:	single
/	TOPOLOGY:	linear
/	FEATURE:	
/	NAME/KEY:	CDS
/	LOCATION:	51..998
/	US-08-378-761A-14	
Query Match		
Best Local Similarity 98.8%; Score 740.8; DB 1; Length 1161;		
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
QY	1	ATGAAAGATAGTGCCTCAGTTTCACGTGAATCTTCCCGTGAGGACGGACTACCCCT 60
Db	51	ATGAAAGATAGTGCCTCAGTTTCACGTGAATCTTCCCGTGAGGACGGACTACCCCT 110
QY	61	TACAGGCCCTTCATCGCGTCCGCGGAAAGACGTGATCAAACTGCACGACCATAAA 120
Db	111	TACAGGCCCTTCATCGCGTCCGCGGAAAGACGTGATCAAACTGCACGACCATAAA 170
QY	121	GGGATCTTCAGCCCCGTGTGCCACCAGGAGAAGTCCCGGAGCTATGGTTTACACA 180
Db	171	GGGATCTTCAGCCCCGTGTGCCACCAGGAGAAGTCCCGGAGCTATGGTTTACACA 230
QY	181	GAACTGAAACTAGGACAGCTCATCACGCTCCGCATAGCATGGACACCTGTACTCT 240
Db	231	GAGCTCAAACACTAGGACAGCTCATCACGCTCCGCATAGCATGGACACCTGTACTCT 290
QY	241	GTGGCTTTCAGGACCCCGGGCGGGGTGTGTGGGAGTTTCGCAAGGACGGCGACACCCAC 300
Db	291	GTGGCTTTCAGGACCCCGGGCGGGGTGTGTGGGAGTTTCGCAAGGACGGCGACACCCAC 350
QY	301	CTCTCTGGCGACAAACCCAGTAGTGGCTTCGGCTTCGGCGCGCAGGTACCAAGGACCTCATCGGC 360
Db	351	CTCTCTGGCGACAAACCCAGTAGTGGCTTCGGCTTCGGCGCGCAGGTACCAAGGACCTCATCGGC 410
QY	361	AACNAGGCTCTGGAGACGGTTCACCATGGGCGCGCCGCAATATGACCAAGGCGCGTCAACGAC 420
Db	411	AACNAGGCTCTGGAGACGGTTCACCATGGGCGCGCCGCAATATGACCAAGGCGCGTCAACGAC 470
QY	421	CTGGCGAAGAGAAAGAGGGCGGCTGACCCACAGGCGCACAGAAAGACAAAGCTGTGAAG 480
Db	471	CTGGCGAAGAGAAAGAGGGCGGCTGACCCACAGGCGCACAGAAAGACAAAGCTGTGAAG 530
QY	481	CTGGTGTGTATGGTGTGCGAGGGGCTGCGGTTTCAACACCGTGTCCCGCACGGTGAAGCGC 540

Db	531	CRGTGGTTCATGGTGTGCGAGGGGCTGCGGTTCAACACCGTGTCCCGCACGGTGGACGCG	590
Qy	541	GGGTTCAACAGCAGCAGCAGCGGGGTGACCTTTGACCGGTGACGCGAGGGGAAGCAGGTGCAGAAG	600
Db	591	GGGTTCAACAGCAGCAGCAGCGGGGTGACCTTTGACCGGTGACGCGAGGGGAAGCAGGTGCAGAAG	650
Qy	601	TGGACAGGATCTCAAGCGCGCCCTTCAGTGGGCTGACCAACCCACACCGTGTGATCCCC	660
Db	651	TGGGACAGGATCTCAAGCGCGCCCTTCAGTGGGCTGACCAACCCACACCGTGTGATCCCC	710
Qy	661	GACATGCAGAAGCTTGGCATCAAGGATGAAGAACGAAGCAGCAGGATCGTTGCCCTCGTT	720
Db	711	GACATGCAGAAGCTTGGCATCAAGGATGAAGAACGAAGCAGGATCGTTGCCCTCGTT	770
Qy	721	AGAATCAAACTACTGCCCGCTGCC	744
Db	771	AGAATCAAACTACTGCCCGCTGCC	794
RESULT 8			
US-08-485-286-14			
; Sequence 14, Application US/08485286			
; Patent No. 5646026			
; Patent No. 5646026 5646119			
; GENERAL INFORMATION:			
; APPLICANT: WALSH, TERENCE A			
; APPLICANT: HEY, TIMOTHY D			
; APPLICANT: MORGAN, ALICE ER			
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE			
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF			
; TITLE OF INVENTION: USING			
; NUMBER OF SEQUENCES: 81			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: ANDREA T. BORUCKI			
; STREET: 9330 ZIONSVILLE ROAD			
; CITY: INDIANAPOLIS			
; STATE: IN			
; COUNTRY: US			
; ZIP: 46268			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/485,286			
; FILING DATE:			
; CLASSIFICATION: 435			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 08/378761			
; FILING DATE: 26-JAN-1995			
; ATTORNEY/AGENT INFORMATION:			
; NAME: BORUCKI, ANDREA T			
; REGISTRATION NUMBER: 33651			
; REFERENCE/DOCKET NUMBER: 38272B			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (317) 337-4846			
; INFORMATION FOR SEQ ID NO: 14:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 1161 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: 51..998			
US-08-485-286-14			

Query Match 98.8%; Score 740.8; DB 1; Length 1161;
Best Local Similarity 99.7%; Pred. No. 3.4e-152;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ATGAAAGAATATGTGCCAAGTTTCATGAAATTCCTCCCGTGGAGAGCGGAACCTACCT 60

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Db 51 ATGAAAGAAATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGACGCAACTACCT 110
QY 61 TACAGCGCTTATCGCTGCTGCGGAAAGAGTGCATCAACACATGACGACCAACATAA 120
Db 111 TACAGCGCTTATCGCTGCTGCGGAAAGAGTGCATCAACACATGACGACCAACATAA 170
QY 121 GGGATCTTCCAGCCCTGCTGCCACCGGAGAAAGTCCCGAGGATATGTTCTACACA 180
Db 171 GGGATCTTCCAGCCCTGCTGCCACCGGAGAAAGTCCCGAGGATATGTTCTACACA 230
QY 181 GAATGAAATAGACACGAGTCCATCACTGCGCATACGATGCGATGACAACTGACCTTAC 240
Db 231 GAGCTCAAACTAGGACGAGTCCATCACTGCGCATACGATGCGATGACAACTGACCTTAC 290
QY 241 GTGGGCTTCCAGACCCCGGCGGGGTGTTGGGAGTTCGGCAAGGACGCGACACCCAC 300
Db 291 GTGGGCTTCCAGACCCCGGCGGGGTGTTGGGAGTTCGGCAAGGACGCGACACCCAC 350
QY 301 CTCCTCGGCGACAAACCCAGGTGGCTCGGCTTCCGCGGAGGTACCGAGACCTCATCGGC 360
Db 351 CTCCTCGGCGACAAACCCAGGTGGCTCGGCTTCCGCGGAGGTACCGAGACCTCATCGGC 410
QY 361 AACAGGGTTCGAGACCGTCAACATGGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCG 420
Db 411 AACAGGGTTCGAGACCGTCAACATGGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCG 470
QY 421 CTGGCGAAGAAAGAGGCGGTGACCCACAGCGCGACACGAGAGCAAGTGGTGAAG 480
Db 471 CTGGCGAAGAAAGAGGCGGTGACCCACAGCGCGACACGAGAGCAAGTGGTGAAG 530
QY 481 CTGGTGGTTCGAGGCGGTGCGGTTCACACACCGTGTCCCGCACGCTGGACGCG 540
Db 531 CTGGTGGTTCGAGGCGGTGCGGTTCACACACCGTGTCCCGCACGCTGGACGCG 590
QY 541 GGGTTCAACAGCCAGCAGCGGGGTGACTTGCCTGACCGTGAACGAGGAGCAAGTGCAGAG 600
Db 591 GGGTTCAACAGCCAGCAGCGGGGTGACTTGCCTGACCGTGAACGAGGAGCAAGTGCAGAG 650
QY 601 TGGGACAGGATCTCCAAAGCGCGCTTCCAGTGGGCTGACCCACCGCCCGCTGTGATCCGC 660
Db 651 TGGGACAGGATCTCCAAAGCGCGCTTCCAGTGGGCTGACCCACCGCCCGCTGTGATCCGC 710
QY 661 GACATGACAGGCTTGGCATCAAGGATAGAAACGAGGAGGATCGTTGCGCTCGTT 720
Db 711 GACATGACAGGCTTGGCATCAAGGATAGAAACGAGGAGGATCGTTGCGCTCGTT 770
QY 721 AAGAATCAAACTACTGCGCTGCC 744
Db 771 AAGAATCAAACTACTGCGCTGCC 794

RESULT 9
US-08-378-761A-16
; Sequence 16, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761A
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1422 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 51..1256
US-08-378-761A-16

Query Match 98.8%; Score 740.8; DB 1; Length 1422;
Best Local Similarity 99.7%; Pred. No. 3.5e-152;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAAGAAATAGTGCACAAAGTTCATCTGAAATCTTCCCGTGGAGACGCAACTACCT 60
Db 51 ATGAAAGAAATAGTGCACAAAGTTCATCTGAAATCTTCCCGTGGAGACGCAACTACCT 110
QY 61 TACAGCGCTTTCATCGCTGCGTCCGAAAGACGTGATCAAAACATGTCACCGACCAATAA 120
Db 111 TACAGCGCTTTCATCGCTGCGTCCGAAAGACGTGATCAAAACATGTCACCGACCAATAA 170
QY 121 GGGATCTTCCAGCCCTGCTGCCACCGGAGAAAGTCCCGAGGATATGTTCTACACA 180
Db 171 GGGATCTTCCAGCCCTGCTGCCACCGGAGAAAGTCCCGAGGATATGTTCTACACA 230
QY 181 GAATGAAATAGACACGAGTCCATCACTGCGCATACGATGCGATGACAACTGACCTTAC 240
Db 231 GAGCTCAAACTAGGACCGTCAACATGGCGCGCGGCTGACCGTGAACGAGGAGCAAGTGG 290
QY 241 GTGGGCTTCCAGACCCCGGCGGGGTGTTGGGAGTTCGGCAAGGACGCGACACCCAC 300
Db 291 GTGGGCTTCCAGACCCCGGCGGGGTGTTGGGAGTTCGGCAAGGACGCGACACCCAC 350
QY 301 CTCCTCGGCGACAAACCCAGGTGGCTCGGCTTCCGCGGAGGTACCGAGACCTCATCGGC 360
Db 351 CTCCTCGGCGACAAACCCAGGTGGCTCGGCTTCCGCGGAGGTACCGAGACCTCATCGGC 410
QY 361 AACAGGGTTCGAGACCGTCAACATGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 420
Db 411 AACAGGGTTCGAGACCGTCAACATGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 470
QY 421 CTGGCGAAGAAAGAGGCGGTGACCCACAGCGCGACACGAGAGCAAGTGGTGAAG 480
Db 471 CTGGCGAAGAAAGAGGCGGTGACCCACAGCGCGACACGAGAGCAAGTGGTGAAG 530
QY 481 CTGGTGGTTCGAGGCGGTGCGGTTCACACACCGTGTCCCGCACGCTGGACGCG 540
Db 531 CTGGTGGTTCGAGGCGGTGCGGTTCACACACCGTGTCCCGCACGCTGGACGCG 590
QY 541 GGGTTCAACAGCCAGCAGCGGGGTGACTTGCCTGACCGTGAACGAGGAGCAAGTGCAGAG 600
Db 591 GGGTTCAACAGCCAGCAGCGGGGTGACTTGCCTGACCGTGAACGAGGAGCAAGTGCAGAG 650
QY 601 TGGGACAGGATCTCCAAAGCGCGCTTCCAGTGGGCTGACCCACCGCCCGCTGTGATCCGC 660
Db 651 TGGGACAGGATCTCCAAAGCGCGCTTCCAGTGGGCTGACCCACCGCCCGCTGTGATCCGC 710
QY 661 GACATGACAGGCTTGGCATCAAGGATAGAAACGAGGAGGATCGTTGCGCTCGTT 720
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Db 711 GACATGCAAGCTTGGCATCAAGGATAAGAAAGCAAGCAGCGAGGATCGTTGGCTCGTT 770
QY 721 AAGAATCAAACTACTGCCGCTGCC 744
Db 771 AAGAATCAAACTACTGCCGCTGCC 794

RESULT 10
US-08-485-286-16
; Sequence 16, Application US/08485286
; Patent No. 5646026
; Patent No. 5646026 5646119
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,286
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/378761
; FILING DATE: 26-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1422 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 51..1256
US-08-485-286-16

Query Match 98.8%; Score 740.8; DB 1; Length 1422;
Best Local Similarity 99.7%; Pred. No. 3.5e-152;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAAGAAATAGTGCAGAGTTCTACTGAAATCTTCCCGTGAGACGCGAACTACCT 60
Db 51 ATGAAAGAAATAGTGCAGAGTTCTACTGAAATCTTCCCGTGAGACGCGAACTACCT 110
QY 61 TACAGCGCTTTCATCGCGTGGTCCGGAAGACGTGATCAAACTGCACCGACCTATAA 120
Db 111 TACAGCGCTTTCATCGCGTGGTCCGGAAGACGTGATCAAACTGCACCGACCTATAA 170
QY 121 GGGATCTTCCAGCCCGTGTGTCGCCACCGGAGAGAGGTCCCGAGCTATGGTTCTACACA 180
Db 171 GGGATCTTCCAGCCCGTGTGTCGCCACCGGAGAGAGGTCCCGAGCTATGGTTCTACACA 230

QY 181 GAACTGAAAACTAGGACGAGCTTCCATCATCGCTCGCCATAGCGATGAGCAAACTGTACCTC 240
Db 231 GAGCTCAAACTAGGACGAGCTTCCATCATCGCTCGCCATAGCGATGAGCAAACTGTACCTC 290
QY 241 GTGGGCTTCAGGACCCCGGGCGGGGTGTGGTGGAGTTCCGGGAAGAGCGGACACCCAC 300
Db 291 GTGGGCTTCAGGACCCCGGGCGGGGTGTGGTGGAGTTCCGGGAAGAGCGGACACCCAC 350
QY 301 CTCCTCGGCGCAAAACCCAGGTGGCTTCGGCTTCGGCGCGAGGTACGAGACCTCATCGGC 360
Db 351 CTCCTCGGCGCAAAACCCAGGTGGCTTCGGCTTCGGCGCGAGGTACGAGACCTCATCGGC 410
QY 361 AACAAAGGGTCTGGAGACCGTCAACCATGGCGCGCGCGGAAATGACACGAGGCCGTCAACGAC 420
Db 411 AACAAAGGGTCTGGAGACCGTCAACCATGGCGCGCGCGGAAATGACACGAGGCCGTCAACGAC 470
QY 421 CTGGCGAAGAGAAAGAGCGGCTGACCCACAGGCGCGACACAGGCGGAGAGTGTGAAG 480
Db 471 CTGGCGAAGAGAAAGAGCGGCTGACCCACAGGCGCGACACAGGCGGAGAGTGTGAAG 530
QY 481 CTGGTGTTCATGGTGTGGAGGGGTGCGGTTCAACACCGTGTCCGCGACGGTGGACGCG 540
Db 531 CTGGTGTTCATGGTGTGGAGGGGTGCGGTTCAACACCGTGTCCGCGACGGTGGACGCG 590
QY 541 GGGTTCAACAGCCAGCAGCGGGGTGACCTTGACCGTGAACGAGGGAAGCAGGTGCAGAG 600
Db 591 GGGTTCAACAGCCAGCAGCGGGGTGACCTTGACCGTGAACGAGGGAAGCAGGTGCAGAG 650
QY 601 TGGGACAGGATCTCAAGCGGCGCTTGGAGTGGGCTGACCCACCGCTGTGATCCCC 660
Db 651 TGGGACAGGATCTCAAGCGGCGCTTGGAGTGGGCTGACCCACCGCTGTGATCCCC 710
QY 661 GACATGCAGAGCTTGGCATCAAGGATAAGAACGAGCAGCAGGATCGTTGCGCTCGTT 720
Db 711 GACATGCAGAGCTTGGCATCAAGGATAAGAACGAGCAGCAGGATCGTTGCGCTCGTT 770
QY 721 AAGAATCAAACTACTGCCGCTGCC 744
Db 771 AAGAATCAAACTACTGCCGCTGCC 794

RESULT 11
US-08-378-761A-18
; Sequence 18, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,761A
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B

ADDRESS: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,286
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/378761
FILING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1695 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 51..1552
US-08-485-286-22

Query Match 98.8%; Score 740.8; DB 1; Length 1695;
Best Local Similarity 99.7%; Pred. No. 3.7e-152;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAAGATAGTGCACAAAGTTCACTGAATCTTCCCGTGAGGACGGAACTACCT 60
DB 51 ATGAAAGATAGTGCACAAAGTTCACTGAATCTTCCCGTGAGGACGGAACTACCT 110
QY 61 TACAGCGCTTCATCGGTCGGTCCGGAAGAAGCTGATCAAACTGCACCGACCAATAA 120
DB 111 TACAGCGCTTCATCGGTCGGTCCGGAAGAAGCTGATCAAACTGCACCGACCAATAA 170
QY 121 GGGATCTTCAGCCCGTGTGCCACCGGAGAAGGTCCCGGAGCTATGGTTCTACACA 180
DB 171 GGGATCTTCAGCCCGTGTGCCACCGGAGAAGGTCCCGGAGCTATGGTTCTACACA 230
QY 181 GAACTGAAAGTACAGGACCTCCATCAGCTGCCATAGCGATGGAACACCTGTACCTC 240
DB 231 GAGCTTAAAGTACAGGACCTCCATCAGCTGCCATAGCGATGGAACACCTGTACCTC 290
QY 241 GTGGGCTTCAGGACCCCGGGGGTGTGGGAGTTCGGCAAGGACGGGACACCCAC 300
DB 291 GTGGGCTTCAGGACCCCGGGGGTGTGGGAGTTCGGCAAGGACGGGACACCCAC 350
QY 301 CTCTCGGACACACCCAGGTGGCTCGGCTTCGGCGGAGTACAGGACCTCATCGG 360
DB 351 CTCTCGGACACACCCAGGTGGCTCGGCTTCGGCGGAGTACAGGACCTCATCGG 410
QY 361 AACAGGCTCTGGAGACCTCACCATAGGGCGCGCCGAAATGACAGCGCGTCAACGAC 420
DB 411 AACAGGCTCTGGAGACCTCACCATAGGGCGCGCCGAAATGACAGCGCGTCAACGAC 470
QY 421 CTGGCGAAGAGAAGAGCGGCTGACCCACAGGCGGACACCAAGAGCAAGCTCGTGAAG 480
DB 471 CTGGCGAAGAGAAGAGCGGCTGACCCACAGGCGGCTGACCCACAGGCGGACACCAAGAGCAAGCTCGTGAAG 530
QY 481 CTGTGGTGTGTTGCGAGGGGTGGGTTTCAACACCGTGTCCCGACCGTGGACGG 540

DB 531 CTGTGGTGTGATGGTGTGCGAGGGGGTCCGGTTCAACCGTGTCCCGACGGTGCACGG 590
QY 541 GGGTTCAACAGCCAGCACGGGGTGACCTTTGACCGGTGACCGGGAAGCAGGTGCAGAAG 600
DB 591 GGGTTCAACAGCCAGCACGGGGTGACCTTTGACCGGTGACCGGGAAGCAGGTGCAGAAG 650
QY 601 TGGGACAGGATCTCAAGGGGGCTTCGAGTGGGTGACACCCACCGCTGTGATCCCC 660
DB 651 TGGGACAGGATCTCAAGGGGGCTTCGAGTGGGTGACACCCACCGCTGTGATCCCC 710
QY 661 GACATGCGAAGCTTGGCATCAAGGATAGAACGAGCAGGAGGATGTTCCGCTCGTT 720
DB 711 GACATGCGAAGCTTGGCATCAAGGATAGAACGAGCAGGAGGATGTTCCGCTCGTT 770
QY 721 AAGAATCAAACTACTGCCGCTGCC 744
DB 771 AAGAATCAAACTACTGCCGCTGCC 794

RESULT 15

US-08-378-761A-24
Sequence 24, Application US/08378761A
Patent No. 5635384
GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
TITLE OF INVENTION: USING
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761A
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1722 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 51..1559
US-08-378-761A-24

Query Match 98.8%; Score 740.8; DB 1; Length 1722;
Best Local Similarity 99.7%; Pred. No. 3.7e-152;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAAGATAGTGCACAAAGTTCACTGAATCTTCCCGTGAGGACGGAACTACCT 60
DB 51 ATGAAAGATAGTGCACAAAGTTCACTGAATCTTCCCGTGAGGACGGAACTACCT 110
QY 61 TACAGCGCTTCATCGGTCGGTCCGGAAGAAGCTGATCAAACTGCACCGACCAATAA 120

Db	111	TACAGCGCTTCATCGCGTCGCTCGGAAAGCGTGATCAAAACACTGCACCGACCATAAA	170
QY	121	GGGATCTTCCAGCCGCTGCTGCCACCGGAGAGAGGTCCCGAGCTATGTTCTACACA	180
Db	171	GGGATCTTCCAGCCGCTGCTGCCACCGGAGAGAGGTCCCGAGCTATGTTCTACACA	230
QY	181	GAACTGAAACTAGGACCAAGCTCCATCAGGCTCGCCATACGATGACCAACCTGTACCTC	240
Db	231	GAGCTCAAACTAGGACCAAGCTCCATCAGGCTCGCCATACGATGACCAACCTGTACCTC	290
QY	241	GTGGGCTTCAGGACCCCGGGGGGTGTGTGGAGTTCTGGCAAGAACCGCGGACACCCAC	300
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QY	421	CTGGCGAAGAGAAAGGCGGCTGACCCACAGGCGGACACGAAAGCAAGCTGGTGAAG	480
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QY	541	GGGTTCAACAGCCAGCACGGGGTGACCTTGACCGTGACGCGGGGAAGCAAGTSCAGAAG	600
Db	591	GGGTTCAACAGCCAGCACGGGGTGACCTTGACCGTGACGCGGGGAAGCAAGTSCAGAAG	650
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QY	661	GACATGCAGAGCTTGGCATCAAGGATAAGAACGAGCAGGAGGATCGTTGCGCTCGTT	720
Db	711	GACATGCAGAGCTTGGCATCAAGGATAAGAACGAGCAGGAGGATCGTTGCGCTCGTT	770
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Db	771	AAGAATCAAACTACTGCCGTGCC	794

Search completed: October 22, 2003, 06:51:36
Job time : 83 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 22, 2003, 05:05:17 ; Search time 2048 Seconds

(without alignments)
8900.565 Million cell updates/sec

Title: US-09-978-273-2

Perfect score: 750

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: em_esthum:*

3: em_estin:*

4: em_estmu:*

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6: em_estpl:*

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8: em_htc:*

9: gb_est1:*

10: gb_est2:*

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12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

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27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	510.8	68.1	1155	11 AY104490	AY104490 Zea mays
3	490	65.3	748	14 CD433123	CD433123 EL01N0304
4	467	62.3	820	29 BZ720403	BZ720403 PUDAV35TD

5	460	61.3	798	14	CD448738	CD448738 EK07D2305
6	438.8	58.5	681	14	CD448132	CD448132 EK07D2303
7	437.4	58.3	752	29	BZ614599	BZ614599 I945d12.9
8	419.2	55.9	600	14	CD439415	CD439415 EL01N0524
9	370.8	49.4	562	10	BF481680	BF481680 FMI_21_A1
C 10	369.6	49.3	846	29	CC332989	CC332989 OGTAH31TV
C 11	348	46.4	672	14	CD448302	CD448302 EK07D2305
C 12	340	45.3	695	14	CD448545	CD448545 EK07D2303
C 13	336.6	44.9	366	14	TI18690	TI18690 5C04F01-T7
C 14	306	40.8	436	9	AI667697	AI667697 605026A04
C 15	306	40.8	573	9	AI664942	AI664942 605004F08
C 16	306	40.8	610	9	AI665398	AI665398 605010G04
C 17	304.4	40.6	522	9	AI833854	AI833854 605096D02
C 18	295	39.3	561	9	AI668230	AI668230 605018E05
C 19	284	37.9	600	10	BF481516	BF481516 FMI_21_A1
C 20	271.2	36.2	527	29	BZ799034	BZ799034 PUFCK38TD
C 21	270.2	36.0	458	14	CA040843	CA040843 EL01N0524
C 22	264.6	35.3	423	9	AW157976	AW157976 za31d10.X
C 23	258.4	34.5	478	28	BH638577	BH638577 1008023D0
C 24	254.8	34.0	515	28	BH414969	BH414969 1007040F0
C 25	244.8	32.6	403	14	T25265	T25265 5cl1d07 mem
C 26	237.6	31.7	576	10	BG559906	BG559906 RHIZ2_75
C 27	236.8	30.2	376	14	TI18677	TI18677 5C04B01-T7
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C 30	215.8	28.8	419	28	BH638701	BH638701 1008024B0
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C 32	215.6	28.7	682	29	BZ614598	BZ614598 I945d12.B
C 33	214.2	28.6	456	14	CA398486	CA398486 EL01N0304
C 34	212	28.3	436	28	BH629418	BH629418 1007072C0
C 35	208.4	27.8	361	9	AI670370	AI670370 605022F01
C 36	190	25.3	460	28	BH629453	BH629453 1007072F0
C 37	180.8	24.1	507	10	BG517901	BG517901 947064D04
C 38	176.8	23.6	450	14	TI18631	TI18631 5C07a12-C7
C 39	176.6	23.5	485	12	BG836402	BG836402 Zm06_01h0
C 40	173	23.1	655	14	CA604530	CA604530 wr1.pk004
C 41	160.8	21.4	391	14	T23398	T23398 5C09d11 mem
C 42	142.2	19.0	318	13	BQ655923	BQ655923 PR00037_S
C 43	129	17.2	271	28	BH628746	BH628746 1007084G0
C 44	128.8	17.2	227	28	BH629588	BH629588 1007073E0
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ALIGNMENTS

RESULT 1	AY109436	AY109436	3101 bp	mRNA	linear	HTC 17-OCT-2002
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DEFINITION	Zea mays	CL1124_1	mRNA sequence.			
ACCESSION	AY109436					
VERSION	AY109436.1	GI:21213157				
KEYWORDS	HTC.					
SOURCE	Zea mays					
ORGANISM	Zea mays					
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD					
AUTHORS	Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.					
TITLE	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes					
JOURNAL	Unpublished (2002)					
REFERENCE	2 (bases 1 to 3101)					
AUTHORS	Coe, E.H.					
TITLE	Direct Submission					
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA					
COMMENT	If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the					

maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES

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/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
BASE COUNT 733 a 565 c 645 g 632 t 526 others
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Matches 714; Conservative 0; Mismatches 27;
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1816 ATCTTCCAGCCGCTGCTGCCACGAGAGAGGTACCGAGCTGTGTTCTACAGGAG 1875
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526 CGCAGGTGGACGCGGGTTCAACAGCCAGCAGCGGGTGACCTTACCGTGAACGAGGG 585
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QY 706 ATCGTTGGCTCGTTAAGATCAAACTACTGCGCGCTGCC 744
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DEFINITION Zea mays PC0148580 mRNA sequence.
ACCESSION AY104490
VERSION AY104490.1 GI:21207568
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1155)
AUTHORS Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
JOURNAL Unpublished (2002)
AUTHORS 2 (bases 1 to 1155)
Coe, E.H.
JOURNAL Direct Submission
TITLE Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSU, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.
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Best Local Similarity 80.7%; Pred. No. 5.2e-106;
Matches 633; Conservative 0; Mismatches 97; Indels 54; Gaps 1;
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QY 121 GGGATCTTCCAGCCGCTGTCCACCGGAGAGAGGTCCCGGAGCTATGTTCTACACA 180
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RESULT 3
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LOCUS             EL01N0304G01.b Endospem_3 Zea mays cDNA, mRNA sequence.
DEFINITION
ACCESSION        CD433123
VERSION          CD433123.1  GI:31348766
KEYWORDS
SOURCE           Zea mays
ORGANISM         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                  clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS          Lai,J., Dey,N., Kim,C.S., Beecraft,P., Larkins,B., Linton,E. and
                  Messing,J
TITLE            Sequencing of the maize endospem ESTs
JOURNAL          Unpublished
COMMENT          Contact: Lai, Jinsheng
                  Dr. Joachim Messing's lab
                  Waksman Institute, Rutgers University
                  190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
                  Tel: 732-445-3801
                  Fax: 732-445-5735
                  Email: jlai@waksman.rutgers.edu
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Best Local Similarity 87.8%; Pred. No. 2.5e-101;
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DEFINITION        genomic survey sequence.
ACCESSION        BZ720403
VERSION          BZ720403.1  GI:28510832
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SOURCE           GSS.
ORGANISM         Zea mays
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                  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                  clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS          Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T., Resnick
                  A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennetzen,J.
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TITLE	Maize Genomics Consortium	CD448738	798 bp	mRNA	linear	EST 03-JUN-2003
JOURNAL	Unpublished	LOCUS	EX07D2305H08.b	Endosperm_6	Zea mays	CDNA, mRNA sequence.
COMMENT	Unpublished	DEFINITION	CD448738			
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		ORGANISM	Zea mays			
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REFERENCE			1 (bases 1 to 798)			
AUTHORS			Lai, J., Dey, N., Kim, C.S., Becraft, P., Larkins, B., Linton, E. and Messing, J.			
TITLE			Sequencing of the maize endosperm ESTs			
JOURNAL			Unpublished			
COMMENT			Contact: Lai, Jinsheng			
			Dr. Joachim Messing's lab			
			Waksman Institute, Rutgers University			
			190 Frelinghuysen Rd., Piscataway, NJ 08854, USA			
			Tel: 732-445-3801			
			Fax: 732-445-5735			
			Email: jlai@waksman.rutgers.edu			
			Seq primer: T3.			
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			Best Local Similarity	87.9%;	Pred. No. 1.7e-94;	
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Db			68	GGGGGCTGTGTGGAGTTTCGGCAAGGACGGCAGCACCTCTCTCGGCAACACCCCA	127	
QY			320	GGTGGCTCGGCTTCGGCGGAGGTACCGAGGACCTCATCGGCAACAAAGGCTCTGGAGACG	379	
Db			128	GGTGGCTCGGCTTCGGCGGAGGTACCGAGGACCTCATCGGCAACAAAGGCTCTGGAGACG	187	
QY			380	TCACCATGGCGCGCGAATGACCGGCGGTCAACGACCTGCGGCAAGAGAGAGAG-	438	
Db			188	TCACCATGGCGCGCGAATGACCGGCGGTCAACGACCTGCGGCAAGAGAGAGAG-	247	
QY			439	-----	438	
Db			248	TGGCACACTGGAGAGGAGGTGCAGATGCAGATCGCGGAGCGCGTGATC	307	
QY			439	-----CCGGCTGACCCACAGGCGGACACGAGAGCAAGCTGTGTGAAGCTGG	484	
Db			308	TGGCGGCGGCGGAGCGGTGACCCACAGGCGGACACGAGAGCAAGCTGTGTGAAGCTGG	367	
QY			485	TGGTCATGTGTCCAGGGGCTGCGGTTCAACACCGTTCGCCGACGCTGACGCGGGGT	544	
Db			368	TGGTCATGTGTCCAGGGGCTGCGGTTCAACACCGTTCGCCGACGCTGACGCGGGGT	427	
QY			545	TCACAGCCAGCACCGGGGTGACCTTTGACCGTACCGCAGGGGAGAGAGTGCAGAAAGTGG	604	
Db			428	TCACAGCCAGCACCGGGGTGACCTTTGACCGTACCGCAGGGGAGAGAGTGCAGAAAGTGG	487	
QY			605	ACAGGATCTTCCAAAGCGGCGCTTCGAGTGGGCTTGAACAACCCACCGCTGTGATCCCCGACA	664	

TITLE	Maize Genomics Consortium	CD448738	798 bp	mRNA	linear	EST 03-JUN-2003
JOURNAL	Unpublished	LOCUS	EX07D2305H08.b	Endosperm_6	Zea mays	CDNA, mRNA sequence.
COMMENT	Unpublished	DEFINITION	CD448738			
	TIGR	ACCESSION	CD448738			
		VERSION	CD448738.1	GI:31364383		
		KEYWORDS	EST.			
		SOURCE	Zea mays			
		ORGANISM	Zea mays			
			Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.			
REFERENCE			1 (bases 1 to 798)			
AUTHORS			Lai, J., Dey, N., Kim, C.S., Becraft, P., Larkins, B., Linton, E. and Messing, J.			
TITLE			Sequencing of the maize endosperm ESTs			
JOURNAL			Unpublished			
COMMENT			Contact: Lai, Jinsheng			
			Dr. Joachim Messing's lab			
			Waksman Institute, Rutgers University			
			190 Frelinghuysen Rd., Piscataway, NJ 08854, USA			
			Tel: 732-445-3801			
			Fax: 732-445-5735			
			Email: jlai@waksman.rutgers.edu			
			Seq primer: T3.			
FEATURES			Location/Qualifiers			
source			1..820			
			/organism="Zea mays"			
			/mol_type="genomic DNA"			
			/strain="B73"			
			/db_xref="taxon:4577"			
			/clone="ZMMBTai45822"			
			/clone_lib="ZM 0.6 1.0 kb"			
			/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high			
			CoT selected genomic DNA library"			
BASE COUNT			197 a 224 c 256 g 143 t			
ORIGIN						
			Query Match	62.3%;	Score 467;	DB 29; Length 820;
			Best Local Similarity	88.0%;	Pred. No. 4.4e-96;	
			Matches	552;	Conservative	0; Mismatches 0; Indels 75; Gaps 1;
QY			193	AGGACAGCTTCATCAGCTCGCCATACGATGACACCTGTACTCTGTGGGCTTCAGG	252	
Db			1	AGGACAGCTTCATCAGCTCGCCATACGATGACACCTGTACTCTGTGGGCTTCAGG	60	
QY			253	ACCCCGGGGGGTGTGTGGAGTTTCGGCAAGGACGGGACACCACTCTCTCGGCGAC	312	
Db			61	ACCCCGGGGGGTGTGTGGAGTTTCGGCAAGGACGGGACACCACTCTCTCGGCGAC	120	
QY			313	AACCCAGGTGTGCTGGCTTCGGCGGAGGTACCGAGGACCTCATCGGCAACAAAGGTCTG	372	
Db			121	AACCCAGGTGTGCTGGCTTCGGCGGAGGTACCGAGGACCTCATCGGCAACAAAGGTCTG	180	
QY			373	GAGACCGTCAACATGGCGCGCGGAAATGACAGGGCGGTCAACGACCTTGGCGAAGAG	432	
Db			181	GAGACCGTCAACATGGCGCGCGGAAATGACAGGGCGGTCAACGACCTTGGCGAAGAG	240	
QY			433	AGAGAG-----	438	
Db			241	AAGAGATGGACACTGGAGAGGAGGAGGTGCAGATGCAGATGCGGAGGCC	300	
QY			439	-----GCGGCTGACCCACAGGCGGACACGAGGCAAGCTGGTG	477	
Db			301	GCTGATCTGGCGGCGGCGAGCGGCTGACCCACAGGCGGACACGAGAGCAAGCTGGTG	360	
QY			478	AGCTGGTGTATGTTGCGAGGGGCTGCGGTTCAACACCGTGTCCGCGACGCTGGAC	537	
Db			361	AGCTGGTGTATGTTGCGAGGGGCTGCGGTTCAACACCGTGTCCGCGACGCTGGAC	420	
QY			538	GCGGGGTTCAACAGCAGACACGGGTTGACCTTGACCGTGCAGCGGGGAGCAGGTGCG	597	
Db			421	GCGGGGTTCAACAGCAGACACGGGTTGACCTTGACCGTGCAGCGGGGAGCAGGTGCG	480	
QY			598	AACTGGGACAGGATCTCCAAAGCGGCTTCGAGTGGGCTGACCAACCCACCGCTGTGATC	657	
Db			481	AACTGGGACAGGATCTCCAAAGCGGCTTCGAGTGGGCTGACCAACCCACCGCTGTGATC	540	
QY			658	CCGACATGCAGAGCTTGGCATCAAGGTAAGAACGAGCAGGAGTTCGTCGCTC	717	
Db			541	CCGACATGCAGAGCTTGGCATCAAGGTAAGAACGAGCAGGAGTTCGTCGCTC	600	
QY			718	GTTAAGAACTCAAACTACTGCCGCTGCC	744	
Db			601	GTTAAGAACTCAAACTACTGCCGCTGCC	627	


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Db      488 ACAGGATCTCCAAAGCGCGCTTCGAGTGGGTGACACCCACCGCTGTGATCCCGACA 547
Qy      665 TCAGAGCTTGGCATCAAGGTAAGAACAGAGCAGCAGGATCGTTGGCGCTCGTTAAGA 724
Db      548 TCAGAGAGCTTGGCATCAAGGTAAGAACAGAGCAGCAGGATCGTTGGCGCTCGTTAAGA 607
Qy      725 ATCAAACTACTGCGCGTGC 744
Db      608 ATCAAACTACTGCGCGTGC 627

RESULT 6
CD448132
LOCUS      CD448132      681 bp      mRNA      linear      EST 03-JUN-2003
DEFINITION EK07D22303A09.g Endosperm_6 Zea mays cDNA, mRNA sequence.
ACCESSION  CD448132
VERSION     CD448132.1 GI:31363775
KEYWORDS   EST.
SOURCE     Zea mays
ORGANISM   Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 681)
AUTHORS   Lai,J., Dey,N., Kim,C.S., Becraft,P., Larkins,B., Linton,E. and
          Messing,J.
TITLE     Sequencing of the maize endosperm ESTs
JOURNAL   Unpublished
COMMENT   Contact: Lai, Jinsheng
          Dr. Joachim Messing's lab
          Waksman Institute, Rutgers University
          190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
          Tel: 732-445-3801
          Fax: 732-445-5735
          Email: jlai@waksman.rutgers.edu
          Seq primer: T7.

FEATURES             Location/Qualifiers
     source           1..681
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                     /mol_type="mRNA"
                     /cultivar="W22"
                     /db_xref="taxon:4577"
                     /tissue type="Endosperm of 7-23 DAP"
                     /clone lib="Endosperm 6"
                     /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT      174 a 189 c 213 g 103 t      2 others
ORIGIN
Query Match      58.5%; Score 438.8; DB 14; Length 681;
Best Local Similarity 94.0%; Pred. No. 1.1e-89;
Matches 455; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy      4 AAAAGAATAGTCCAAAGTTCACTGAATCTTCCCGTGGAGAGCGCGAACTACCTTAC 63
Db      101 AAAAGAATAGTCCAAAGTTCACTGAATCTTCCCGTGGAGAGCGCGAACTACCTTAC 160
Qy      64 AGCGCTTCATCGCTCGCTCCGGAAGACGTTGATCAAAACACTGCACCGACCAATAAAGG 123
Db      161 AGCGCTTCATCGCTCGCTCCGGAAGACGTTGATCAAAACACTGCACCGACCAATAAAGG 220
Qy      124 ATCTTCAGCCCGTGTGTCACCGAGAGAAAGGTCCCGAGCTATGTTCTACACAGAA 183
Db      221 ATCTTCAGCCCGTGTGTCACCGAGAGAAAGGTCCCGAGCTATGTTCTACACAGAG 280
Qy      184 CTGAAACTAGGACACAGCTCCATCAAGCTCGGCATACGATGACAACTGTACCTCGTG 243
Db      281 CTGAAACTAGGACACAGCTCCATCAAGCTCGGCATACGATGACAACTGTACCTCGTG 340
Qy      244 GCCTTCAGACCCCGCGGGGTGTGGTGGAGTTCGGCAAGCAGCGGCACACCCACCTC 303
Db      341 GGCTTCAGACCCCGCGGGGTGTGGTGGAGTTCGGCAAGCAGCGGCACACCCACCTC 400

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Qy      304 CTCGGCGCAAAACCCAGGTGGCTCGGCTTCGGCGGCAGGTACCGAGCACTCATCGGCAAC 363
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Qy      364 AAGGTTCTGGAGACCGTCCACCATGGCGCGCCGAAATGACCGAGGCGCGTCAACGACCTG 423
Db      461 AAGGTTCTGGAGACCGTCCACCATGGCGCGCCGAAATGACCGAGGCGCGTCAACGACCTG 520
Qy      424 CGGAGAGAAAGAGGCGGCTGACCCACAGCCCGACACGAAGAGCAAGCTGCTGAAGCTG 483
Db      521 CGGAGAGAAAGAGATGGCGCACTGGAGGAGGAGGAGTGCANATGCANATGCAGATG 580
Qy      484 GTGG 487
Db      581 CCGG 584

RESULT 7
BZ614599
LOCUS      BZ614599      752 bp      DNA      linear      GSS 16-JAN-2003
DEFINITION ig45dl12.g1 WGS-ZmaysF (DH5a methyl filtered) Zea mays genomic clone
ACCESSION  BZ614599
VERSION     BZ614599.1 GI:27765154
KEYWORDS   GSS.
SOURCE     Zea mays
ORGANISM   Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 752)
AUTHORS   Rabinowicz,P.D., O'Shaughnessy,A.L., Balija,V., Dedhia,N.,
          Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,
          Zutavern,T., McCombie,W.R. and Martienssen,R.A.
          Genomic shotgun sequences from Zea mays (methyl-filtered)
          Unpublished
          Contact: W. Richard McCombie
          Lita Annenberg Hazen Genome Sequencing Center
          Cold Spring Harbor Laboratory
          PO Box 100, Cold Spring Harbor, NY 11724, USA
          Tel: 516 367 8884
          Fax: 516 367 8874
          Email: mcombie@cshl.org
          Plate: ig45 row: d column: 12
          Seg primer: -21M13UnivRev
          Class: shotgun
          High quality sequence stop: 752.
          Location/Qualifiers
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                             /db_xref="taxon:4577"
                             /lab host="DH5a"
                             /clone="ig45dl12"
                             /note="WGS-ZmaysF (DH5a methyl filtered)"
                             The vector was digested with XbaI and one nucleotide was
                             added by fill in the recessive 3' end. The genomic DNA
                             was nebulized, end repaired, adaptor ligated and size
                             fractionated using sephadex. The resulting fragments were
                             between 0.8 and 3 kb and were cloned into the vector (.x/y
                             reads in M13mpl9, .b/g reads in pUC19). The same ligation
                             was transformed into DH5a."
BASE COUNT      180 a 215 c 237 g 120 t
ORIGIN
Query Match      58.3%; Score 437.4; DB 29; Length 752;
Best Local Similarity 79.3%; Pred. No. 2.4e-89;
Matches 556; Conservative 0; Mismatches 91; Indels 54; Gaps 1;

Qy      84 CCGGAAAGACGTTGATCAAAACACTGCACCGACCAATAAAGGATCTTCCAGCCGCTGCTGCC 143

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Db 24 CTTCCGAGGAGTGATCAAAATACGTCCACCAACCATACAGGATCGTCCAGCCCGTGCTGCC 83
QY 144 ACCGAGAGAGAGTCCCGAGCTATGTTCTTACACAGAACTCAAACTAGGACCAAGCTC 203
Db 84 GTTGGAGAAGATGTCCTCCGAGCTCTGGTTCTACACGAGCTCAAAACGAAGACAGGTC 143
QY 204 CATCAGCTCGCCATACGATGATGACAACTGTACCTCGTGGGCTTCAGGACCCCGGGCGG 263
Db 144 CATCAGCTCGCCATACGATGATGACAACTGTACCTCGTGGGCTTCAGGACCCCGGGCGG 203
QY 264 GTTGTGGTGGAGTTCCGCAAGACCGGCAACCCACCTCTCGGGCAACACCCCAAGTGT 323
Db 204 GTTGTGGTGGAGTTCCGCAAGACCGGCAACCCACCTCTCGGGCAACACCCCAAGTGT 263
QY 324 GTTGTGGTGGAGTTCCGCAAGACCGGCAACCCACCTCTCGGGCAACACCCCAAGTGT 383
Db 264 GTTGTGGTGGAGTTCCGCAAGACCGGCAACCCACCTCTCGGGCAACACCCCAAGTGT 323
QY 384 CATGGCCCGCGCGAATGACAGGCGCGTCAACGACCTGGCGAAGAAAGAAAG----- 438
Db 324 CATGGCCCGCGCGAATGACAGGCGCGTCAACGACCTGGCGAAGAAAGAAAG----- 383
QY 439 -----GCGGCTGACCC 449
Db 384 ACTAGCAGAGGCGCGAGGAGGAGGAGGAGTCTGCTGCTCAGGACGCGCTGACCC 443
QY 450 ACAGGCGCGACACGAAGCAAGCTGTGAAGCTGTGTGTCATGTTGTGCGAGGGGCTGG 509
Db 444 CAAGCCGAGGAGAGAGCAACTGGCGAAGCTGTGATGATGATGATGCGAGGGGCTGG 503
QY 510 GTTCAACACCGTGTCCCGCAGCGTGGACGCGGGGTTCAACAGCAGCAGCGGCTGACCTT 569
Db 504 GTTCTTACCGTGTCCCGCAAGTGTAGACGAGGGTTCAAGAGCGCGAAGCGGTGACCAT 563
QY 570 GACCGTGACGAGGAGACAGTGTGAGAGTGGAGCAGGATCTCAAGCGCGCTTCA 629
Db 564 ATCGCGCTGGAGGGGAGCAGGTGAGAAATGGGACAGGATCTCGAAGCGCTCTTCAG 623
QY 630 GTGGGCTGACACCCCGCTGTATCCCGCATGTCAGAGAGCTTGGCATCAAGATTA 689
Db 624 GTGGGCTGACACCCCGCTGTATCCCGCATGTCAGAGAGTCTTGGCATCAAGATTA 683
QY 690 GAACGAAGCAGCAGGATCGTTGCGCTCGTTAAGATCAAA 730
Db 684 AAACGAGCTGCGCAGATCGTTGCGCTCGTTAAGACCAA 724
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RESULT 8
CD439415 600 bp mRNA linear EST 03-JUN-2003
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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```
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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Sequencing of the maize endospERM ESTs
Lai, J., Dey, N., Kim, C.S., Becraft, P., Larkins, B., Linton, E. and
Messing, J.
Unpublished
Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
Seq primer: 17.
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FEATURES

Location/Qualifiers

source

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1. 600
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="W22"
/db_xref="taxon:4577"
/tissue_type="EndospERM of 7-23DAP"
/clone_lib="EndospERM 5"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"
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BASE COUNT 139 a 168 c 207 g 86 t

Query Match 55.9%; Score 419.2; DB 14; Length 600;
Best Local Similarity 85.3%; Pred. No. 3.1e-85;
Matches 512; Conservative 0; Mismatches 13; Indels 75; Gaps 1;

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QY 97 ATCAAACTGCACGACCATAAAGGATCTTCCAGCCCGTCTGCCACCGGAGAAAG 156
Db 1 ATCAAACTGCACGACCATAAAGGATCTTCCACGAGCTGCCACCGGAGAAAG 60
QY 157 GTCCCGGAGCTATGTTCTACACAACTGAAAACCTAGACCAAGCTCATCACTCGCC 216
Db 61 GTCCCGGAGCTATGTTCTACACAGCTCAAACTAGACCAAGCTCATCACTCGCC 120
QY 217 ATACGATGGACAACCTGTACTCTGTGGCTTTCAGGACCCCGGGCGGGTGTGGGAG 276
Db 121 ATACGATGGACAACCTGTACTCTGTGGCTTTCAGGACCCCGGGCGGGTGTGGGAG 180
QY 277 TTCCGAAGGAGCGGCGACACCCACCTCTCGGCGACAACCCAGGTGGTTCGGCTTCGCG 336
Db 181 TTCCGAAGGAGCGGCGACACCCACCTCTCGGCGACAACCCAGGTGGTTCGGCTTCGCG 240
QY 337 GCGAGTACAGGACCTCATCGCAAGAGGTCTGGAGACCGTCAATGGGCGCGCC 396
Db 241 GCGAGTACCACTATTTCATCGCAAGAGGTCTGGAGACCGTCAATGGGCGCGCC 300
QY 397 GAAATGACAGGCGCGTCAACGACCTGCGGAGGAGAAAG----- 438
Db 301 GAAATGACAGGCGCGTCAACGACCTGCGGAGGAGAAAGAGATGGCGACACTGGAGGAG 360
QY 439 -----GCG 441
Db 361 GAGGAGTGCAGATGCAGATCGGAGGCGCGTGTCTGTGGCGCGCGCGAGG 420
QY 442 GTGACCCACAGGCGCGACACGAGCAAGCTGTGTAAGCTGTGCTCATGTGTGCGAG 501
Db 421 GTGACCCACAGGCGCGACACGAGCAAGCTGTGTAAGCTGTGCTCATGTGTGCGAG 480
QY 502 GGGCTGCGGTTCAACACCGTGTCCCGCACGCTGGACGCGGTTTCAACAGCCAGCACGG 561
Db 481 GGGCTGCGGTTCAACACCGTGTCCCGCACGCTGGACGCGGTTTCAACAGCCAGCACGG 540
QY 562 GTGACCTTGCAGCTGACGCGGAGGAGCAGGTGAGAAAGTGGAGCAGGATCTCCAAGCG 621
Db 541 GTGACCTTGCAGCTGACGCGGAGGAGCAGGTGAGAAAGTGGAGCAGGATCTCCAAGCG 600
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RESULT 9
BF481680

LOCUS

DEFINITION

propinquum cDNA, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Sorghum propinquum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 562)

Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M., Marsala, C. and Pratt

, L.H.

TITLE An EST database from Sorghum: floral-induced meristems
 JOURNAL Unpublished
 COMMENT Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmpratt@uga.edu
 Sequences have been trimmed to exclude PolyA, vector and regions
 below Phred quality 16. The threshold for highest quality sequence
 is 20.
 Seq primer: JEN REV
 High quality sequence stop: 498
 POLYA-No.

FEATURES

source Location/Qualifiers

1..562
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 /mol_type="mRNA"
 /db_xref="taxon:132711"
 /clone_lib="Floral-Induced Meristem 1 (FM1)"
 /note="Organ: Floral-induced meristems; Vector:
 pBluescript II from lambda Zap II; Site 1: XhoI; Site 2:
 EcoRI; mature plants were placed in a growth chamber for
 15 days with 16 hr darkness and 8 hr light (flowering is
 induced by short-day conditions); 16 days after being
 returned to the greenhouse under natural long days during
 late April/early May, meristems were harvested. The
 library was made from poly-A RNA in the cloning vector
 lambda Zap II. Clones to be sequenced were prepared by
 mass excision."

BASE COUNT 151 a 160 c 154 g 97 t

Query Match 49.4%; Score 370.8; DB 10; Length 562;
 Best Local Similarity 90.4%; Pred. No. 3.2e-74;
 Matches 396; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 1 ATGAAAGAAAGTCCCAAGTTCTACTGAATCTCCCGGTGGAGCGCACTACCT 60
 Db 87 AAGAAAAAATAGTACCAAGTTCTACTGAAACCTTCCCGGTGGAGCGTACCT 146
 Qy 61 TACAGCGCTTCATCGCTCGGTCCGGAAGAGCTGATCAACACTGCACCGACCAATAA 120
 Db 147 TACGCTCTTCATCGCGCGGTGAGAAAGATGGTCAATATCTGCACCGCAATAA 206
 Qy 121 GGGATCTTCCAGCCCGTCTGCCACCGAGAGAAAGTCCCGGAGCTATGTTCTACACA 180
 Db 207 GGCATCTTCCAGCCTGTCTGCCCGCGGAGAGAGTCCCGGAGCTCTGTTCTACACC 266
 Qy 181 GAACCTGAAACTAGGACCACTCCATCAGCTCGCCATACGATCGGCAACCTGTACCTC 240
 Db 267 CAGCTCAAAACCAAGACCACTCCATCAGCTCGCCATACGATCGGCAACCTGTACCTC 326
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 Db 387 CTCCTCGACGCAACCCAGGTGGTCTGGCTTCGGCGGAGGTACAGGACCTCATCGGC 446
 Qy 361 AACAGGCTTCAGAACCTGACCATGGCCCGCGGAAATGACAGGCGGTCAACGAC 420
 Db 447 AATAAGGGCTTCAGAACCTGACCATGGCCCGGTGGCGCGGTGGCGGAGGTCAACGAC 506
 Qy 421 CTGGCGAAGAAAGAG 438
 Db 507 CTGGCGAAGAACGACG 524

RESULT 10
 CC332989/c

LOCUS CC332989 846 bp DNA linear GSS 16-MAY-2003
 DEFINITION OCTAH31TV_ZM_0_7_1.5_KB_Zea_mays_genomic_clone_ZM5BMA0388F14,
 genomic survey sequence.

ACCESSION CC332989
 VERSION CC332989.1 GI:30802272
 KEYWORDS GSS.

SOURCE Zea mays
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 846)

REFERENCE Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick
 A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek
 R.W., Nunberg,A., Robbins,D. and Lakey,N.
 Consortium for Maize Genomics

TITLE Unpublished
 JOURNAL Contact: Cathy Whitelaw
 COMMENT TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@tigr.org

Seq primer: TF
 Class: sheared ends.

FEATURES Location/Qualifiers

1..846
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 /strain="B73"
 /db_xref="taxon:4577"
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 /clone_lib="ZM_0_7_1.5_KB"
 /note="Vector: pACSK-; Site 1: KincII; 0.7-1.5 kb
 methylation filtered genomic DNA library"

BASE COUNT 160 a 253 c 226 g 207 t

Query Match 49.3%; Score 369.6; DB 29; Length 846;
 Best Local Similarity 78.3%; Pred. No. 6.6e-74;
 Matches 481; Conservative 0; Mismatches 79; Indels 54; Gaps 1;

Qy 171 GTTCTACACAGAACTGAAACTAGACACAGCTCCATCAGCTCGCCATACCATGGACAA 230
 Db 837 GTTCTACACGAGCTCAAACAGACAGAGTCCATCAGCTCGCCATACCATGGACAA 778
 Qy 231 CCTTACTCTGTGGCTTCAGGACCCCGGGCGGGTGTGTGGAGTTCGGCAAGGACG 290
 Db 777 CCTTACTCTGTGGCTTCAGGACCCCGGGCGGGTGTGTGGAGTTCGGCAAGGACG 718
 Qy 291 CGACACCACTCTCTCGGCGACAACCCAGGTGCTCGGCTTCGGCGGAGTACCAGGA 350
 Db 717 CGACACCACTCTCTCGGCGACAACCCAGGTGCTCGGCTTCGGCGGAGTACCAGGA 658
 Qy 351 CCTCATCGGCAACAAGGTTCTGGAGACCGTCCATGGGCGCGCGCAAAATGACAGGCG 410
 Db 657 CCTCATCGGCAAGTAAAGGCTTCGAGACCGTCCATGGGCGCGCGCAAAATGACAGGCG 598
 Qy 411 CGTCAACGACCTGCGGAAGAGAGAGAG----- 438
 Db 597 CGTCAACTACTCTGGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 538
 Qy 439 -----GCGGCTGACCCACAGCCGCGTACCCCAAGCCGAGAGAGAGAGAGAGAGAGAG 476
 Db 537 GGAGCTGCTGCTGTGCGAGGCGCGGTGACCCCAAGCCGAGAGAGAGAGAGAGAGAGAG 478
 Qy 477 GAAGCTGTGTGTATGTGTGCGAGGGGCTTCGGTTCACACCGTGTCCCGACCGGTGA 536
 Db 477 GAAGCTGTGTATGTGTATGTGCGAGGGGCTTCGGTTCACACCGTGTCCCGACCGGTGA 418
 Qy 537 CGCGGGTTCAACAGCCGAGCGGGGTGACCTTACCGTGCAGCGGAGAGAGAGAGAGAGAG 596
 Db 417 CGAGGGGTTCAAGAAAGCGCAAGCGGTGACCATATCGCGCGCTGGAGGGGAGAGAGAGAG 358

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QY 597 GAAGTGGACAGGATCTCAAGCGGCTTCGAGTCGGCTGACACCCACCGCTGTGAT 656
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QY 657 CCCCAGCATGCGAAGCTTGGCATCAAGGATAGAACGACGAGGATCGTTGCGCT 716
|||
Db 297 CCCCAGCATGAGGATCTTGGCATCAAGATAAACGACGCTGCGCAGATCGTTGCGCT 238
|||
QY 717 CGTTAAGATCAAA 730
|||
Db 237 CGTTAAGACCAA 224
|||

CD448302 672 bp mRNA linear EST 03-JUN-2003
LOCUS EK07D2305H08.g EndospERM_6 Zea mays cDNA, mRNA sequence.
CD448302
DEFINITION
ACCESSION CD448302
VERSION
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS Lai,J., Dev,N., Kim,C.S., Becraft,P., Larkins,B., Linton,E. and
Messing,J.
TITLE Sequencing of the maize endospERM ESTs
JOURNAL Unpublished
COMMENT Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
Seq primer: T7.

FEATURES
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BASE COUNT 106 a 212 c 176 g 178 t

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Best Local Similarity 85.2%; Pred. No. 5.1e-69;
Matches 433; Conservative 0; Mismatches 0; Indels 75; Gaps 1;

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RESULT 12
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ACCESSION CD448545
VERSION
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS Lai,J., Dev,N., Kim,C.S., Becraft,P., Larkins,B., Linton,E. and
Messing,J.
TITLE Sequencing of the maize endospERM ESTs
JOURNAL Unpublished
COMMENT Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
Seq primer: T3.

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 QY 725 ATCAAACTACTGCGGCTGCC 744
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 ACCESSION T18690
 VERSION T18690.1 GI:485620
 KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 366)
 Shen, B., Carneiro, N., Torres-Jerez, I., Stevenson, R., McCreery, T., Helentjaris, T., Baysdorfer, C., Almira, E., Ferl, R., Habben, J. and Larkins, B.
 Partial sequencing and mapping of clones from two maize cDNA libraries
 Plant Mol. Biol. 26, 1085-1101 (1994)
 95111093
 7811968
 Contact: The Maize cDNA Project

Helentjaris TG (primary contact)
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Rob Ferl
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 DNA Sequencing Core
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 P.O. Box 100695
 Gainesville, FL 32611-0695
 ph: 904-392-1928, ext. 301
 fax: 904-392-4072

E-mail: roberlnervm.nerdc.ufl.edu

Seq primer: T7
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 Best Local Similarity 98.3%; Pred. No. 1.7e-66;
 Matches 350; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
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 DEFINITION cDNA, mRNA sequence.
 ACCESSION A1667697
 VERSION A1667697.1 GI:4826069
 KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 436)
 Maize ESTs from various cDNA libraries sequenced at Stanford
 Walbot, V.
 AUTHOR TITLE
 JOURNAL
 COMMENT

Unpublished
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University

WALBOT, V.
 Maize ESTs from various cDNA libraries sequenced at Stanford
 TITLE
 JOURNAL
 COMMENT
 Unpublished
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 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2327

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OM nucleic - nucleic search, using sw model

Run on: October 22, 2003, 06:15:45 ; Search time 282 Seconds
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7132.449 Million cell updates/sec

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Perfect score: 750
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1792395 segs, 1340900451 residues

Total number of hits satisfying chosen parameters: 3584790

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : Published Applications NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	307.4	41.0	354	10	US-09-978-273-4
5	113.8	15.2	240	9	US-09-294-093B-1275
6	77.6	10.3	846	12	US-10-127-890-12
7	55.6	7.4	2340	9	US-09-815-242-7995
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	31	48.4	6.5	4350	14	US-10-168-843A-33	Sequence 33, Appl
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	43	47.2	6.3	1083	14	US-10-156-761-4116	Sequence 4116, Ap
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ALIGNMENTS

RESULT 1

US-09-978-273-2
; Sequence 2, Application US/09978273
; Patent No. US20020138869A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: Plant Cell Death System
; FILE REFERENCE: 9341-037
; CURRENT APPLICATION NUMBER: US/09/978, 273
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
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; ORGANISM: Zea mays
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; NAME/KEY: misc feature
; LOCATION: (1)..(3)
; OTHER INFORMATION: Initiation codon added via PCR primer
; NAME/KEY: mutation
; LOCATION: (181)..(186)
; OTHER INFORMATION: Sequence replacing removed SacI site
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; LOCATION: (745)..(750)
; OTHER INFORMATION: Stop codons added by PCR primer
US-09-978-273-2

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Best Local Similarity 100.0%; Pred. No. 2.2e-195;

Matches 750; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Patent No. US20020138869A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: Plant Cell Death System
; FILE REFERENCE: 9341-027
; CURRENT APPLICATION NUMBER: US/09/978,273
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 909
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
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; OTHER INFORMATION: C-terminal Domain
; NAME/KEY: misc feature
; LOCATION: (484)..(558)
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; OTHER INFORMATION: Sequence replacing removed SacI site
; NAME/KEY: misc feature
; LOCATION: (1)..(3)
; OTHER INFORMATION: Initiation codon added via PCR primer
; NAME/KEY: misc feature
; LOCATION: (904)..(909)
; OTHER INFORMATION: Stop codons added via PCR primer
; NAME/KEY: misc feature
; LOCATION: (1)..(24)
; OTHER INFORMATION: Binding site for primer ProRIPBF
; NAME/KEY: misc feature
; LOCATION: (205)..(249)
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Best Local Similarity 90.8%; Pred. No. 1.1e-169;
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Db 109 AGCGCTTCAATCGCGTGGTCCGGAAGACGTGATCAAAACACTGCAACGACATAAAGG 168
QY 124 ATCTTCCAGCCCGTCTGCCACCGGAGAGAGGTCCCGGAGCTATGTTCTACACAGAA 183
Db 169 ATCTTCCAGCCCGTCTGCCACCGGAGAGAGGTCCCGGAGCTATGTTCTACACAGAA 228
QY 184 CTGAAAACTAGGACCAAGCTCCATCAAGCTCGCATACGATGGAACCACTGTACCTCGT 243
Db 229 CTGAAAACTAGGACCAAGCTCCATCAAGCTCGCATACGATGGAACCACTGTACCTCGT 288
QY 244 GCGTTACGAGACCCCGCGGGGTGTGTGGAGTTCGGCAAGGACGGCGACACCCACCTC 303
Db 289 GCGTTACGAGACCCCGCGGGGTGTGTGGAGTTCGGCAAGGACGGCGACACCCACCTC 348
QY 304 CTCGGGACAAACCCAGGTGGCTCGGCTTCCGGCGGAGTACCGAGGACCTCATCGGCAAC 363
Db 349 CTCGGGACAAACCCAGGTGGCTCGGCTTCCGGCGGAGTACCGAGGACCTCATCGGCAAC 408
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QY 556 CACGGGTGACCTTGACCGGTGACGCGAGGGAACAGAGTGCGAGAGTGGGACAGATCTCC 615
Db 121 CACGGGTGACCTTGACCGGTGACGCGAGGGAACAGAGTGGGACAGATCTCC 180
QY 616 AAGCGGCGCTTCGAGTGGGCTGACCCACCGCTGTGATCCCGACATGCGAGAGCTT 675
Db 181 AAGCGGCGCTTCGAGTGGGCTGACCCACCGCTGTGATCCCGACATGCGAGAGCTT 240
QY 676 GGCATCAAGGATGAAGAACAGGAGGAGGATCGTTCGCGCTCGTTAAGATCAAACTACT 735
Db 241 GGCATCAAGGATGAAGAACAGGAGGAGGATCGTTCGCGCTCGTTAAGATCAAACTACT 300
QY 736 GCGCTGCCC 744
Db 301 GCGGCTGCC 309

RESULT 5
US-09-294-093B-1275
; Sequence 1275, Application US/09294093B
; Patent No. US20010051335A1
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath, V.
; APPLICANT: Ito, Laura, Y.
; APPLICANT: Sherman, Bradley, K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
; FILE REFERENCE: PL-0009 US
; CURRENT APPLICATION NUMBER: US/09/294,093B
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/082,567
; PRIOR FILING DATE: April 21, 1998
; NUMBER OF SEQ ID NOS: 6207
; SOFTWARE: PERL Program
; SEQ ID NO 1275
; LENGTH: 240
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700344050H1
US-09-294-093B-1275

Query Match 15.2%; Score 113.8; DB 9; Length 240;
Best Local Similarity 87.9%; Pred. No. 1.7e-21;
Matches 124; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 ATGAAAGAAATAGTGCAGAAAGTTCACTGAAATCTTCCCGTGAGGAGCGGAACCTACCCCT 60
Db 100 AAGAAAATATAGTGCCAAAGTTCCAGAAACCTTCCCGTTGAGGACACGGCCTACCCCT 159
QY 61 TACAGCGCTTCAATCGCGTGGTCCGGAAGAGAGTGAATCAAAACATGCAACCGACCAATAA 120
Db 160 TACAGCGCTTCAATCACTCCGTCGCGAAGAGAGTGAATCAAAATGTCACCAACCATACA 219
QY 121 GGCATCTCCAGCCCGTGTG 141
Db 220 GGCATCTCCAGCCCGTGTG 240

RESULT 6
US-10-127-890-12
; Sequence 12, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Studnika, Gary M.
; Carroll, Stephen F.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
```

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; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/10/127,890
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70-P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 12:
; LENGTH: 846 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-127-890-12

Query Match 10.3%; Score 77.6; DB 12; Length 846;
Best Local Similarity 51.2%; Pred. No. 1.6e-11;
Matches 309; Conservative 0; Mismatches 259; Indels 36; Gaps 4;

QY 15 GCCTAAGTTCACTGAAATCTTCCCGTGAGGAGCGGAACTACCTTACAGCGCCTTCAT 74
Db 33 GCGGCTCTTTCACCGGACGTTCAAGCTCCAGGCCAGCTCCGCGGACTAGCCACCTTCAT 92
QY 75 CCGCTCGTCCGGAAGAGCTGATCAA-----ACACTGCAGCGACCAATAAGGATCTT 128
Db 93 CCGCGGATCCGCAACAAGCTCCGCAACCGCGGCACTTCTCCCAACCGCCCGCTGT 152
QY 129 CCAGCCCGTGTCTCCACCGGAGAGAGGTCCCGGAGCTATGTTCTACACAGAACTGAA 188
Db 153 GCGCGGCTCGAGCCCAAGCTCCCGCGAGAGTGTTCACGCTCGTCTCAAGGCCTC 212
QY 189 AACTAGGACAGCTCCATCAGCTCGCATAGCATGCAACCTGTACCTCGTGGGTT 248
Db 213 GCGGACCAAGCGCGGGCTCAAGCTCGCATCCGCGGACACATCTACTTGGAGGGTT 272
QY 249 CAGGACCCCGGCGGGTGTGTGGAGTTCGGCAAGGACGCGGACACCCACTCTCGG 308
Db 273 CAAGACGACGACGCACTGTGTGGAGCT-----CACTCCCGGCTCAT 317
QY 309 CGACAAACCCAGTGGCTTCGGGCGGAGGTACCGAGGACCTCATCGGCAACAAGG 368
Db 318 CCGCGGCGCACCTACGTGGGTTTGGGGGACCTTACCGGACCTCTCTCGGACACCGA 377
QY 369 TCTGGAGACCGTCAACATGGGCGCG-----GCCGAAATGACAGGCGCGCTCAA 416
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Db 378 CAAGCTAACCAAGTCTCTCGCCGACACGACGCTGCGCGACGCGGTGACCGGCTCCA 437
QY 417 CGACCTGGCGAAGAGAGGCGGTGACCCACAGCGCGACACAGAGAGCAAGCTGGT 476
Db 438 CGGGCGACCAAGCCGACAGGCTCGGCGCCGAACAGCAGCAGCGGAGAGGCGGT 497
QY 477 ---GAGCTGGTGTATGTGTGCGAGGCGGTGCGGTCAACACCGTGTCCGCGAGGT 533
Db 498 GACGACGCTGGTCTCTATGTGTGAACAGAGGCGCACGCGGTCCAGACGGTGTCTGGGTTCGT 557
QY 534 GGCAGCGGGGTTCAACAGCAGCAGCGGGTGACCTTGACCGTACCGCAGGAGAGAGGT 593
Db 558 GCGCGGGTTCGTGACCCCAAGCGGTGGAGAAAGAGCGGGAAGATCGGCAATGAGAT 617
QY 594 GCAG 597
Db 618 GAAG 621

RESULT 7

US-09-815-242-7995
; Sequence 7995, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: BLITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-05-23
; PRIOR FILING DATE: 2000-05-23
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-10-23
; PRIOR FILING DATE: 2000-11-27
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2001-02-16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7995
; LENGTH: 2340
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2340)
US-09-815-242-7995

Query Match 7.4%; Score 55.6; DB 9; Length 2340;
Best Local Similarity 44.5%; Pred. No. 2e-05;
Matches 220; Conservative 0; Mismatches 274; Indels 0; Gaps 0;
QY 66 CGCCTTCATCGCTCGGTCCGGAAGAGCTGATCAACACTGACCGACCATAAAGGAT 125
Db 1542 CGGCCTCAACTCGACGCTGGCGGAGAAACATCGTCGGCGACCGCGAGCGCAACGAGCGGT 1601
QY 126 CTTCAGCCCGTCTGCTCCACCGGAGAGAGGTCCCGGAGCTATGTTCTACACAACT 185

Db 1602 CCSCACCCCGCAGAGCTCAAGAAAGTCAAGCCGCTCGGCGAAAGACCTTCGAGCAAGC 1661
QY 186 GAAACTAGGACAGCTCCATCAGCTCGCCATAGCATAGGACAACTGTACCTCGTGGG 245
Db 1662 CGCGGGTCTCTCGGTGTATGAACCGGCGACAACCCGCTGGAGCGCTCGGCGGTGCAACC 1721
QY 246 CTTTCAGAACCCCGGGGGGTGTGTGGAGTTTCGGAAGAGCGGAGACACCCACCTCCT 305
Db 1722 GGAGACTATCCGCTGTGTCAGCGCATCGCGCCGACACCGAGCGGACATCCGCTCGCT 1781
QY 306 CGCGGACACCCAGTGGCTCGGCTTCGGCGGACGTTACAGGACCTCATCGGACAA 365
Db 1782 GATCGGCGACTCGGCGCTTCTCAAGCGCTTCGACCGGAAAGATTCCACGACGAGACCTT 1841
QY 366 GGTCTCTGGAGACGTCACCATGGCGCGCGGAAATGACAGCGGCGTCAACGACCTGGC 425
Db 1842 CGGCTTGGCGACCGTCAACGACATCTCAAGGACTTCGACAGCCCGCGCGACCCGCG 1901
QY 426 GAAGAAAGAGGCGGCTGACCCAGGCGCGACAGAGCAAGCAAGCTGGTGAAGCTGGT 485
Db 1902 TCCGGAGTTCAAGACCGCAGAAATTCAGGAAGCGCTCGAGAGCTCAAGACCTCAAGCC 1961
QY 486 GGTCTATGGTTCGAGGCGGCTCGGTTCAACACCGTGTCCGACAGCTGAGACCGGGGTT 545
Db 1962 GGGCATGGTCTCGAGGCGGTGGTGACCAACGTCACCAACTTCGGGCGGTTCTGTCGACAT 2021
QY 546 CAACAGCCAGCAGC 559
Db 2022 CGCGTCCACAGG 2035

RESULT 8

US-10-156-761-1179
; Sequence 1179, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1179
; LENGTH: 1299
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1299)
US-10-156-761-1179

Query Match 7.4%; Score 55.4; DB 14; Length 1299;
Best Local Similarity 46.2%; Pred. No. 2.1e-05;
Matches 222; Conservative 0; Mismatches 256; Indels 3; Gaps 1;
QY 198 CAGCTTCATCAGCTCGCCATACGATGACAACTGTCTGTGGGTTTCAGGACCCC 257
Db 522 CATCTTCTACAGGCGGAGCACCAACCAACAGATCGTCCCGGCGCTCGACTACTCAA 581
QY 258 GGGCGGGGTGTGTGGAGTTTCGGAAGACGCGGCGACACCACTCTCTGGGCGAACCC 317
Db 582 GAGCCAGGCAAGAAAGATCTACTGTGCGAGCGACTACGTCTTCCCGCGCACCGC 641


```
RESULT 11
US-10-205-032-1
; Sequence 1, Application US/10205032
; Publication No. US20030113874A1
; GENERAL INFORMATION:
; APPLICANT: Farnet, Chris
; APPLICANT: Yang, Xianshu
; APPLICANT: Staffa, Alfredo
; TITLE OF INVENTION: GENES AND PROTEINS FOR THE BIOSYNTHESIS OF ROSARAMICIN
; FILE REFERENCE: 3016-2US
; CURRENT APPLICATION NUMBER: US/10/205,032
; PRIOR FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 60196
; TYPE: DNA
; ORGANISM: micromonospora carbonacea subspecies aurantiaca
US-10-205-032-1
Query Match 7.3%; Score 54.4; DB 14; Length 60196;
Best Local Similarity 49.6%; Pred. No. 7.6e-05;
Matches 139; Conservative 0; Mismatches 141; Indels 0; Gaps 0;
QY 288 CGCGACACCCACCTCTCTGGGACAAACCCACAGTGGCTTGGGGGGGACGATACCA 347
DB 39750 CGCGCGACCGCGCGCTCGCGCGCACGTCGTGGCCCGCGGCTTGGCCCGCGCGCGCGCG 39809
QY 348 GGAACCTCATCGGCAACAAAGGCTCTGGAGACCGTCACCATGGCGCGCGCGCGCGCGCGCG 407
DB 39810 GGAACCTCTGCTCATCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 39869
QY 408 GCGCGTCAACGACCTCTGGGACAAAGAGAGGCGGTGACCCACAGCGCGCGCGCGCGCGCG 467
DB 39870 GGAACCTCGCGCGCTGGGCGCGCGAGGTGACCGTCTGGCGGTCTGGAGCTGCGCGCGCG 39929
QY 468 CAACTGGTGAAGTGGTGGTCTATGTTGCGAGGGGCTGCGGTTCAACACCGTGTCCCG 527
DB 39930 CCGCGTGGCGCGCTCTCTCGCGGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 39989
QY 528 CACGTTGGACGGGGGTTCAACAGCGACGACGCGGGTGACC 567
DB 39990 CACCGCGCGGTGGCGACATCGATGCCGATCGCGGAGACC 40029
RESULT 12
US-10-156-761-2499
; Sequence 2499, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2499
; LENGTH: 5487
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(5487)
US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1
Query Match 6.9%; Score 52; DB 14; Length 9025608;
Best Local Similarity 47.5%; Pred. No. 0.00082;
Matches 191; Conservative 0; Mismatches 205; Indels 6; Gaps 1;
QY 184 CTGAAACTAGGACGAGCTTCATCGCTCGCATCGCATCGCATCGCATCGCATCGCATCG 243
DB 2986 CTGGAGCTGAAGACCAACATCAACAGATGGTGGACCACTGTCTCTTCTGCTGAAGAG 3045
QY 244 GGCCTCAGAACCCCGGGCGGGTGTGGTGGAGTTGGGCAAGACGCGACACCCACCTC 303
DB 3046 GTCAACCGAGTCTCGCCCGGAGGTGGGCAACCGAGGGGCGAGCTGGGGCGGCGAGCG 3105
QY 304 CTCGGCGACAAACCCAGGTGGCTTCGGCTTCGGCGGCGAGTACCGAGACCTCATCGGCAAC 363
DB 3106 CGGAGCTCGACGGACCTGGCGGCGACCTCAACGATCGGTGAACGAGATGGCGCGGGAAC 3165
QY 364 AAGGGTCTGGAGACCGTCAACCATGGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 423
DB 3166 CTGACCGGCGAGTCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 3225
QY 424 GCGAAGAAAGAAAGGCGGCTGACCCACAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 483
DB 3226 AACCTTGAAGATCGAGCTGGAGCGCCTCG-----GGCGAGATCCAGGAACCTTCAGGACTAC 3279
QY 484 GTGGTCATGTTGGAGGGGCTGGGTTTCAACACCGTGTCCGCGACGCGTGGACGCGGGG 543
DB 3280 ATCAACAGATGATCGCNAACCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3339
QY 544 TTCAACAGCCAGCAGGGGTGACCTTGACCGGTGACCGGTGACCGGAGGGG 585
DB 3340 CTCAAGGGCAATCTCGCCCGGATCTCGGCGCTGATGCGAGGGG 3381
RESULT 13
US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1
Query Match 6.9%; Score 52; DB 14; Length 9025608;
Best Local Similarity 47.5%; Pred. No. 0.00082;
Matches 191; Conservative 0; Mismatches 205; Indels 6; Gaps 1;
QY 184 CTGAAACTAGGACGAGCTTCATCGCTCGCATCGCATCGCATCGCATCGCATCGCATCG 243
DB 3066453 CTGGAGCTGAAGACCAACCATCAACAGATGGTGGAGGAGCTGTCTCTTCTGCTGAAGAG 3066394
```

QY 244 GGTTTCAAGACCCCGGCGGGTGTGTGGAGATTTCGCAAGACCGCGACACCCACCTC 303
Db 3066393 GTCAACCGAGTCCCGCGAGGTGGGCAACGAGGGCAGCTGGCGGCGAGGCACGCTG 3066334
QY 304 CTCGGCGCAACCCAGGTGGCTCGGTTTCGGCGGCGAGGTACAGGACCTCATCGGAAC 363
Db 3066333 CGGGAGCTCGACGCGACCTTGGCGGACCTCACCGAGTTCGGTGAACGAGATGGCCGGGAAC 3066274
QY 364 AAGGGTCTGGAGACCGTCAACATGGCGCGCGGAAATGACAGGCGCGTCAACGACCTG 423
Db 3066273 CTGACCGGAGGTGGCGGCATCGCGGCTGCGACCGCGGTGACCCCGCGGACCTG 3066214
QY 424 GCGAAGAAAGAGCGGCTGACCCACAGCGCGCACAGAGCAAGCTGTGAAGCTG 483
Db 3066213 AACCTGAAGATCGACGTGAGCGCTCG-----GGCGAGATCCAGGAACCTTCAGGACTAC 3066160
QY 484 GTGGTATGTGCGAGGGGCTCGGTTCAACACCGTGTCCCGCAGGTGAGCGGGG 543
Db 3066159 ATCAACAAGATGATCGCAACCTTGGCGGACACCAACCATCGCCCAAGGAACAGGACTGG 3066100
QY 544 TTCAACAGCGCAGCAGCGGTGACCTTGACCGTGACGCGAGGGG 585
Db 3066099 CTCAGGGCAATCTCGCCCGATCTCGCCCTGATCGAGGG 3066058

RESULT 14

US-09-846-590B-17
; Sequence 17, Application US/09846590B
; Patent No. US2002009801A1
; GENERAL INFORMATION:
; APPLICANT: Falco, S. Carl
; APPLICANT: Famodu, Layo O.
; APPLICANT: Orozco, Emil M. Jr.
; TITLE OF INVENTION: Amino Acid Decarboxylases
; FILE REFERENCE: BB-1237
; CURRENT APPLICATION NUMBER: US/09/846, 590B
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 60/099,493
; PRIOR FILING DATE: 1998-09-08
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 17
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-846-590B-17

Query Match 6.9%; Score 51.8; DB 9; Length 1377;
Best Local Similarity 47.5%; Pred. No. 0.0002;
Matches 223; Conservative 0; Mismatches 237; Indels 9; Gaps 2;
QY 196 ACCAGCTCCATACGCTCGCCATGACATGGAACCTGTACCTGCTGGGCTTCAGGAC 255
Db 700 AGCGATCTCGGCGAGTCAACCGACCTCAAGGATCGAGTGGCGCTCGCGCCGCTTC 759
QY 256 CCGGG---CGGGGTGTGGTGGAGTTTCGCAAGACGCGGACACCCACCTCTCTCGCGGAC 312
Db 760 CCGGGGCTCAAGTCTGTGATGTGTCATGCGCACCTACGCGCGCGGCAAGCTGCAGGAGCAC 819
QY 313 AACCCAGGTGGTTCGGCTTCGCGGCGAGGTACAGGACCTCATCGGCAACAGGTTCTG 372
Db 820 ATCCGAGGCAAGCTCGCCATGCGCAAGAGCTTCAGGACCTCTGCGCGCGCGACCGG 879
QY 373 GAGACCGTCAACATGGCGCGCGGAAATGACAGGCGCGTCAACGACCTGGCGGAGAG 432
Db 880 TTCGAGTCTGTGTGCGGAGAACTTCGCGCTCTGTCTCTAGGATCAGGCCGAGAA 939
QY 433 AAGAAGCGGCTGACCCACAGGCGGACAGAGAGCAAGCTGTGAAGTGTGTGTCATG 492
Db 940 TCGGCGCGCCCATCGCGCGCGGAGGCGGAGAGCGCAAGCGCAACCGGAGCTGATG 999
QY 493 GTGTGCGAGGGCTGGGGTTCAACACCGTGTCCCGCACGGTGGACCGGGGGTTCAACAGC 552

Db 1000 -----GAGCGGTGAACAAGACCGGAAAGGTTACGTGGCGCACACCGTGGTGGCGGC 1053
QY 553 CAGCAGGGGTACCTTGACCGGTGACGCGAGGGAAGCAGGTGAGAGTGGGACAGATC 612
Db 1054 AGTTCTGTCTGGCTTCGCGGTGGGTCTGCTGCAAGGAGGCGGACGTCGGAAGC 1113
QY 613 TCCAGGCGCGCTTCGAGTGGGTGACCAACCCACCGCTGTGTATCCCG 661
Db 1114 GGTGGGACTCATCAAGAAGACGACCGAGATGTCGCCGACGCCG 1162

RESULT 15

US-10-205-032-15
; Sequence 15, Application US/10205032
; Publication No. US20030113874A1
; GENERAL INFORMATION:
; APPLICANT: Farnet, Chris
; APPLICANT: Yang, Xianshu
; APPLICANT: Staffa, Alfredo
; TITLE OF INVENTION: GENES AND PROTEINS FOR THE BIOSYNTHESIS OF ROSARAMICIN
; FILE REFERENCE: 3016-2US
; CURRENT APPLICATION NUMBER: US/10/205,032
; CURRENT FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 11238
; TYPE: DNA
; ORGANISM: micromonospora carbonacea subspecies aurantiaca
US-10-205-032-15

Query Match 6.8%; Score 51.2; DB 14; Length 11238;
Best Local Similarity 45.0%; Pred. No. 0.00043;
Matches 191; Conservative 0; Mismatches 233; Indels 0; Gaps 0;
QY 201 CTCATATACGCTTCGCGCATACGATGACAACTGTACTCTGTGGCTTCAGGACCCCGG 260
Db 5487 CGCCATGATGTGTGTCAGCGGCTCGCGACCGGAGGCGCGGCGACAGATCTCTGC 5546
QY 261 CGGGGTGTGTGGAGTTGCGCAAGGACGCGGACACCCACCTCTCTGGGCAACCCCG 320
Db 5547 CGTGTCAAGGCTCGCGCTCAACGAGGACGCGGCGGCAACCGGCTCACCGCCCGAA 5606
QY 321 GTGGCTCGGCTTCGCGCGCAGGTACGAGACCTCATCGGCAACAAGGCTTCGAGACCGT 380
Db 5607 CCGGCCCTCCAGGAACGGTTCATCGGCGAGGCTTGCCCGACGCGGCTTCGGCCGGA 5666
QY 381 CACCATGGGCGCGCGGAAATGACAGGCGCGTCAACGACCTTGGCGAAGAAAGAGGC 440
Db 5667 CCAGGTGGACGCGGTGAGGCGCACCGGACCGGACCGGCGGCGGCGGCGGCGGCGG 5726
QY 441 GCTGACCCACAGGCGGACACGAAAGCAGTGTGTGAGTGTGGTTCATGGTGGCA 500
Db 5727 GCAGGCGTGTCTGCGCACGTACGCGCGGACCGGCGGCGGCGGCGGCGGCGGCGG 5786
QY 501 GGGGCTGGGGTTCAACACCGTGTCTCCGCAAGGTGACGCGGGGTTCAACAGCCAGCAG 560
Db 5787 CTCGTTGAATCCACATCGGTCAACCCAGGCGCGCGGCGGCGGCGGCGGCGGCGG 5846
QY 561 GGTGACCTTGAACGTCAGCGGGAAGCAGGTGAGAGTGGGACAGATCTCAAGGC 620
Db 5847 GGTGATCTTGGGCTGCGGCGACGACGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 5906
QY 621 GCCC 624
Db 5907 GCCC 5910

Search completed: October 22, 2003, 08:06:27
Job time : 306 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 22, 2003, 04:06:58 ; Search time 284 Seconds
(without alignments)
7128.798 Million cell updates/sec

Title: US-09-978-273-2

Perfect score: 750

Sequence: 1 atgaaagaatagtgccaaa.....ctactgcgctgctaataa 750

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq_19Jun03.*
1: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
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11: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
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23: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*
25: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	750	100.0	750	24	AA038057
2	740.8	98.8	847	18	AA079869
3	740.8	98.8	847	13	AA077761
4	740.8	98.8	978	13	AA020478
5	740.8	98.8	978	18	AA079864
6	740.8	98.8	978	18	AA077756
7	740.8	98.8	984	18	AA079863
8	740.8	98.8	985	18	AA077755

9	740.8	98.8	1161	18	AA079866	Pro-ribosome inact
10	740.8	98.8	1161	18	AA077758	RIP fusion protein
11	740.8	98.8	1422	18	AA079867	Pro-ribosome inact
12	740.8	98.8	1422	18	AA077759	RIP fusion protein
13	740.8	98.8	1683	13	AA020482	Maize RIP deriv. R
14	740.8	98.8	1683	18	AA079868	Pro-ribosome inact
15	740.8	98.8	1683	18	AA077760	RIP fusion protein
16	740.8	98.8	1695	18	AA079870	Pro-ribosome inact
17	740.8	98.8	1695	18	AA077762	RIP fusion protein
18	740.8	98.8	1722	18	AA079871	Pro-ribosome inact
19	740.8	98.8	1722	18	AA077763	RIP fusion protein
20	739.2	98.6	1422	13	AA020481	Maize RIP deriv. R
21	737.8	98.4	1029	18	AA079862	Maize single chain
22	737.8	98.4	1029	18	AA077754	RIP fusion protein
23	736.6	98.2	1161	13	AA020480	Maize RIP deriv. R
24	720.2	96.0	986	18	AA079865	Truncated pro-ribo
25	720.2	96.0	986	18	AA077757	RIP fusion protein
26	707.4	94.3	987	13	AA020479	Maize KRIP derivat
27	707.2	94.3	987	20	AA078467	Maize KRIP derivat
28	656	87.5	909	24	AA038056	Maize pro-ribosome
29	655.8	87.4	1074	18	AA079873	Maize ribosome ina
30	654.2	87.2	1059	20	AA078470	Maize RIP-2 DNA.
31	652.8	87.0	1076	18	AA079861	Maize pro-ribosome
32	652.8	87.0	1105	13	AA020477	proRIP coding sequ
33	652.8	87.0	1105	18	AA079872	Maize proRIP sequ
34	652.8	87.0	1105	13	AA020477	Maize pro-ribosome
35	652.6	87.0	1053	20	AA078473	Maize RIP-3 DNA.
36	651.2	86.8	1076	13	AA020476	Maize proRIP. Zea
37	649.8	86.6	944	20	AA078475	Maize RIP-4 DNA.
38	649.8	86.6	1244	20	AA078479	Maize RIP-5 DNA.
39	636.8	84.9	1245	20	AA078481	Maize KRIP DNA. Z
40	510.8	68.1	1934	17	AA042302	Maize ribosomal in
41	438	58.4	444	24	AA038058	Maize ribosome ina
42	308	41.1	533	20	AA078489	Maize KRIP 3'-end
43	307.4	41.0	354	24	AA038059	Maize ribosome ina
44	113.8	15.2	240	24	ABL71901	Corn tassal-derive
45	77.6	10.3	846	14	AA042301	Barley Type 1 ribo

ALIGNMENTS

RESULT 1
AA038057
ID AAD38057 standard; DNA; 750 BP.

XX AC AAD38057;

XX AC AAD38057;

DT 10-SEP-2002 (first entry)

XX Maize processed ribosome inactivating protein (RIP-P) encoding DNA.

DE DE Maize; transgenic; transgenic plant; ribosome inactivating protein; RIP;

XX Maize; transgenic; transgenic plant; ribosome inactivating protein; RIP;

KW cytotoxicity; nematode resistant plant; sterility; fruit abscission;

KW viral infection; nematocide; antiviral; RIP-P DNA; ds.

XX Zea mays.

OS Zea mays.

XX Key

XX Key

FT misc_signal

FT Location/Qualifiers

FT 1..3

FT /tag= a

FT /note= "Initiation codon added by PCR primer"

FT misc_feature

FT 181..186

FT /tag= b

FT /note= "sequence replacing removed SacI site"

FT misc_signal

FT 745..750

FT /tag= c

FT /note= "Stop codons added by PCR primer"

FT WO200233106-A2.

XX 25-APR-2002.

PD 25-APR-2002.

XX RIP fusion protein

PF 15-OCT-2001; 2001WO-0B04581.
XX
PR 14-OCT-2000; 2000GB-0025225.
XX
PA (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
PI Thomas CJR, McPherson MJ, Atkinson HJ, Neelam A;
XX
DR WPI; 2002-452390/48.
XX
XX
PT Producing transgenic plant resistant to nematode infection, comprises
PT transforming plant with chimeric gene having promoter inducible at
PT nematode feeding site, linked to sequence encoding maize ribosome
PT inactivating protein
XX
PS Claim 7; Page 85; 89pp; English.
XX
CC The present invention relates to a novel method for producing transgenic
CC plants which harbour chimeric genes within the genome of the plant, the
CC expression of which gene causes plant cytotoxicity at a target site. The
CC method involves transforming a plant with a chimeric gene comprising a
CC promoter inducible at and/or adjacent to a target site, operably linked
CC to a coding sequence encoding a maize ribosome inactivating protein (RIP)
CC or its portion. The method is useful for producing transgenic plants
CC harbouring within the genome a chimeric gene which when expressed,
CC produces a cytotoxic protein. The target site may be a nematode feeding
CC site and by targeting the nematode feeding site, nematode resistant
CC plant can be obtained. If the target site is one or more of plant's
CC pollen, anther or tapetum, the method is useful for effecting the male
CC sterility in plants and if the target site is ovule of plant, the method
CC is directed to effecting female sterility in plants. The target site may
CC be specific parts of the flower or abscission zone of the leaf and/or
CC fruit and the method is useful for manipulating morphology of the flower
CC of a plant and to assist in or promote leaf and/or fruit abscission in
CC plants. The method is also useful for controlling viral infection. The
CC present sequence is maize processed RIP (RIP-P) DNA.
XX
SQ Sequence 750 BP; 185 A; 217 C; 232 G; 116 T; 0 other;
Query Match 100.0%; Score 750; DB 24; Length 750;
Best Local Similarity 100.0%; Pred. No. 7.1e-150;
Matches 750; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAAGAATAGTGCACAAAGTTCACTGAATCTTCCCGTGAGAGCGCAACTACCT 60
Db 1 ATGAAAGAATAGTGCACAAAGTTCACTGAATCTTCCCGTGAGAGCGCAACTACCT 60
QY 61 TACAGCGCTTCATCGCGTGGTCCGGAAGAGTGTATCAAACTGACCGGACCATAA 120
Db 61 TACAGCGCTTCATCGCGTGGTCCGGAAGAGTGTATCAAACTGACCGGACCATAA 120
QY 121 GGGATCTTCAGCGCGTGTGTCACCGGAGAGAGTCCCGGAGCTATGTTCTACACA 180
Db 121 GGGATCTTCAGCGCGTGTGTCACCGGAGAGAGTCCCGGAGCTATGTTCTACACA 180
QY 181 GAATGAAACTAGGACCGAGTCCATCACTGCGCATAGCATGCAACCTGTGACCTC 240
Db 181 GAATGAAACTAGGACCGAGTCCATCACTGCGCATAGCATGCAACCTGTGACCTC 240
QY 241 GTGGGCTTCAGGACCGCGGCGGGTGTGTGGAGTTCGGCAAGGACGCGACCCAC 300
Db 241 GTGGGCTTCAGGACCGCGGCGGGTGTGTGGAGTTCGGCAAGGACGCGACCCAC 300
QY 301 CTCTCGCGCAACACCCAGTGGCTCGGCTTCGGCGGACAGGTACAGGACCTCATCGGC 360
Db 301 CTCTCGCGCAACACCCAGTGGCTCGGCTTCGGCGGACAGGTACAGGACCTCATCGGC 360
QY 361 AACAAAGGTCTGAGACCGTCAACATGGCGCGCGCAATGACCGAGGCGGTCAACGAC 420
Db 361 AACAAAGGTCTGAGACCGTCAACATGGCGCGCGCAATGACCGAGGCGGTCAACGAC 420
QY 421 CTGCGGAGAGAGAGAGGCGGTGACCCACAGCGGACACGAGGACGCTGGTGAAG 480

Db 421 CTGGCCAAAGAGAGAGAGCGCGCTACCCACAGGCCGACAGAGCAAGCTGTGTGAAG 480
QY 481 CTGGTGGTTCATGTTGGAGGGGCTGGGGTTCAACACCGTGTCCCGCACGCTGGACGCG 540
Db 481 CTGGTGGTTCATGTTGGAGGGGCTGGGGTTCAACACCGTGTCCCGCACGCTGGACGCG 540
QY 541 GGGTTCAACAGCAGCAGCGGGGTGACCTTGACCGTGAACGAGGAGCAGGTGAGAAG 600
Db 541 GGGTTCAACAGCAGCAGCGGGGTGACCTTGACCGTGAACGAGGAGCAGGTGAGAAG 600
QY 601 TGGGACAGGATCTCCAAAGCGGCTTCGAGTGGGTGAGTACCCACCGCTGTGATCCCC 660
Db 601 TGGGACAGGATCTCCAAAGCGGCTTCGAGTGGGTGAGTACCCACCGCTGTGATCCCC 660
QY 661 GACATGCGAAGCTTTGGCATCAAGGATGAAGAACGAGCAGCGAGGATCGTTCGGTCTGTT 720
Db 661 GACATGCGAAGCTTTGGCATCAAGGATGAAGAACGAGCAGCGAGGATCGTTCGGTCTGTT 720
QY 721 AAGAATCAAACTACTGCGCGCTGCCTAATAA 750
Db 721 AAGAATCAAACTACTGCGCGCTGCCTAATAA 750
RESULT 2
AAT79869
ID AAT79869 standard; DNA; 847 BP.
XX
AC AAT79869;
XX
DT 25-MAR-2003 (updated)
DT 01-DEC-1997 (first entry)
XX
DE Pro-ribosome inactivating protein gene clone RDT-BHSR.
XX
KW Maize; proRIP; ribosome inactivating protein; alpha; beta subunit;
KW internal linker; Barley Translation Inhibitor; Trichosanthin;
KW Ricin A-chain; Abrin-A chain; Saporin; SLT-1; Luffin A; MAP;
KW Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30;
KW therapeutic toxin; tumour cell targeted; protein synthesis inhibitor;
KW post-translational modification; cancer; neoplasia; HIV; AIDS;
KW human immunodeficiency virus; acquired immune deficiency syndrome; ss.
XX
OS Zea mays.
XX
FH Key Location/Qualifiers
CDS 51..845
FT /*tag= a
FT /*note= "no stop codon given"
XX
PN US5646026-A.
XX
PD 08-JUL-1997.
XX
PF 07-JUN-1995; 95US-0485286.
XX
PR 09-DEC-1992; 92US-0987927.
PR 11-JUN-1990; 90US-0535636.
PR 26-JAN-1995; 95US-0378761.
PR 07-JUN-1995; 95US-0485286.
XX
PA (DOWC) DOWELANCO.
XX
PI Hey TD, Morgan AER, Walsh TA;
XX
DR WPI; 1997-362934/33.
DR P-PSDB; AAN25131.
XX
PT DNA encoding pro-ribosome inactivating proteins - inactive
PT precursors of ribosome inactivating proteins; can be expressed in
PT eukaryotic cells without causing cell death
XX
PS Claim 2; Column 73-76; 186pp; English.

CC AAT79869 encodes a single chain maize pro-ribosome inactivating protein (proRIP). The sequence was engineered to allow the introduction of a synthetic linker separating the alpha and beta units of the RIP protein to form an inactive form of RIP. When separated the two units regain activity and are capable of inactivating eukaryotic ribosomes and hence preventing protein production. Many different Panacoidae RIPs may be produced with an internal linker including: Barley Translation Inhibitor, Trichosanthin, Ricin A-chain, Abrin-A A-chain, Saporin, SLT-1, Luffin A, MAP, Ricinus communis agglutinin, Momordin, PAP-S, Luffin-B and Dianthin 30. The RIPs can be used in the construction of therapeutic toxins targeted to specific cells such as tumour cells via the attachment of a targeting polypeptide, e.g. a monoclonal antibody. A further use is in HIV therapy (see US4869903). There is interest in expressing RIP recombinantly in host eukaryotic cells, because of the capacity to provide correct post-translational processing. However, RIPs effectively inhibit protein synthesis in eukaryotic cells resulting in cell death. Since the proRIP proteins are not cytotoxic to eukaryotic cells, they can be recombinantly expressed in such cells and then converted to active RIP proteins. CC (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 847 BP; 212 A; 240 C; 254 G; 141 T; 0 other;

Query Match 98.8%; Score 740.8; DB 18; Length 847;
Best Local Similarity 99.7%; Pred. No. 6.5e-148;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAAGAAATAGTGCMAAGTTCACTGAATCTTCCCGTGAGAGCGGAACACTACCT 60
DB |||||||
QY 51 ATGAAAGAAATAGTGCMAAGTTCACTGAATCTTCCCGTGAGAGCGGAACACTACCT 110
DB |||||||
QY 61 TACAGCGCCTTATCGCGTCCGTTCCGGAAGACGTGATCAAACTGCACCCGACATAA 120
DB |||||||
QY 111 TACAGCGCCTTATCGCGTCCGTTCCGGAAGACGTGATCAAACTGCACCCGACATAA 170
DB |||||||
QY 121 GGGATCTTCAGCCCGTGTCCACCGGAGAAAGTCCCGAGAGTATGGTTCTACACA 180
DB |||||||
QY 171 GGGATCTTCAGCCCGTGTCCACCGGAGAAAGTCCCGAGAGTATGGTTCTACACA 230
DB |||||||
QY 181 GAACTGAAACTAGGACCACTCCATCAGCTCCGATCGCATGACGACCTGTACCTC 240
DB |||||||
QY 231 GAGCTCAAACTAGGACCACTCCATCAGCTCCGATCGCATGACGACCTGTACCTC 290
DB |||||||
QY 241 GTGGGCTTCAGGACCCCGCGGGGTGTGGTGGAGTTGGCAAGGACGCGCACCCAC 300
DB |||||||
QY 291 GTGGGCTTCAGGACCCCGCGGGGTGTGGTGGAGTTGGCAAGGACGCGCACCCAC 350
DB |||||||
QY 301 CTCCTCGGCGACAAACCCAGGTGGTTCGGTTCGGCGGAGTACAGGACCTCATCGG 360
DB |||||||
QY 351 CTCCTCGGCGACAAACCCAGGTGGTTCGGTTCGGCGGAGTACAGGACCTCATCGG 410
DB |||||||
QY 361 AACAGGGTCTTGAGACCGGTCACTATGGCGCGCGGAAATGACAGGGCGGTCAACGAC 420
DB |||||||
QY 411 AACAGGGTCTTGAGACCGGTCACTATGGCGCGCGGAAATGACAGGGCGGTCAACGAC 470
DB |||||||
QY 421 CTGGCGAAGAAAGAGCGGCTGACCCACAGCGCGACACGAAAGACGAAGTGTGAAG 480
DB |||||||
QY 471 CTGGCGAAGAAAGAGCGGCTGACCCACAGCGCGACACGAAAGACGAAGTGTGAAG 530
DB |||||||
QY 481 CTGGTGTCTATGTGTGCGAGGGGCTCGGTTCAACACCGTGTCCGCGAGTGGACGG 540
DB |||||||
QY 531 CTGGTGTCTATGTGTGCGAGGGGCTCGGTTCAACACCGTGTCCGCGAGTGGACGG 590
DB |||||||
QY 541 GGGTTCAACAGCCAGCACCGGGGTGACCTTGACCGTGAACGAGGGGAGAGGTGCAAG 600
DB |||||||
QY 591 GGGTTCAACAGCCAGCACCGGGGTGACCTTGACCGTGAACGAGGGGAGAGGTGCAAG 650
DB |||||||
QY 601 TGGGACAGGATCTCCAGGGCGGCTTCAGTGGGCTGACACCCACCGGTGTGATCCCC 660
DB |||||||
QY 651 TGGGACAGGATCTCCAGGGCGGCTTCAGTGGGCTGACACCCACCGGTGTGATCCCC 710
DB |||||||
QY 661 GACATCAGAGCTTGGCATCAGGATAGAAAGAGCAGGAGGATCGTTGGCGCTCGTT 720
DB |||||||

Db 711 GACATGCAGAGCTTGCCATCAAGGATAAGAAAGCAGCAGGAGTCTTGCGCTCGTT 770
QY 721 AAGAATCAAACTACTGCCGCTGCC 744
Db 771 AAGAATCAAACTACTGCCGCTGCC 794

RESULT 3
AAT77761
ID AAT77761 standard; DNA; 847 BP.
XX
AC AAT77761;
XX
DT 25-MAR-2003 (updated)
DT 26-SEP-1997 (first entry)
XX
DE RIP fusion protein, RDT-BHSR coding sequence.
XX
KW pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer;
KW inactivation; eukaryotic ribosome; alpha fragment; beta fragment;
KW inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver;
KW rat; ribosomal 28S RNA; cellular proliferation; HIV-infected T cell; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
CDS 51..845
FT /*tag= a
FT /product= RDT-BHSR
XX
PN US5635384-A.
XX
XX 03-JUN-1997.
XX
XX 26-JAN-1995; 95US-0378761.
XX
XX 09-DEC-1992; 92US-0987927.
PR 11-JUN-1990; 90US-0535636.
PR 26-JAN-1995; 95US-0378761.
XX
XX (DOWC) DOWELANCO.
XX
XX Hey TD, Morgan AER, Walsh TA;
PI
XX WPI; 1997-309831/28.
DR P-PSDB; AAM21718.
XX
PT Inactive precursor of maize ribosome-inactivating protein - also
PT chimeric ribosome-inactivating protein precursors containing
PT internal linker sequences
XX
PS Claim 4; Column 73-76; 121pp; English.
XX
XX The sequences given in AAT77754-63 encode fusion proteins which are
XX examples of Ribosome Inactivating Proteins. RIPs are potent inhibitors
XX of eukaryotic protein synthesis. They possess a highly specific
XX N-glycosidase activity which cleaves the glycosidic bond of adenine
XX 4324 of rat liver ribosomal 28S RNA. RIP's selectively inhibit
XX cellular proliferation of cells, e.g. cancer cells and HIV-infected
XX T cells. The inactive proRIP proteins make it possible to provide
XX protein synthesis inhibitors with uses in practical and improved
XX ways not before possible. The RIP can be used to make cytotoxic
XX conjugates.
XX (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 847 BP; 212 A; 240 C; 254 G; 141 T; 0 other;

Query Match 98.8%; Score 740.8; DB 18; Length 847;
Best Local Similarity 99.7%; Pred. No. 6.5e-148;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAAGAAATAGTGCMAAGTTCACTGAATCTTCCCGTGAGAGCGGAACACTACCT 60
|||||

Db 51 ATGAAAAGTAAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGGACGCGAACTACCT 110
Qy 61 TACAGCGCTTCATCGCTCGTTCGGGAAAGACGTGATCAAAACACTGACACCATATAA 120
Db 111 TACAGCGCTTCATCGCTCGTTCGGGAAAGACGTGATCAAAACACTGACACCATATAA 170
Qy 121 GGGATCTTCAGCGCTTCGTCACCGGAGAAAGGTCCTCGGAGCTATGTTTACACA 180
Db 171 GGGATCTTCAGCGCTTCGTCACCGGAGAAAGGTCCTCGGAGCTATGTTTACACA 230
Qy 181 GAACTGAAACTAGACACGCTCCATCAGCTCGCCATACGATGACAACTGTTACCTC 240
Db 231 GAGCTCAAACTAGACACGCTCCATCAGCTCGCCATACGATGACAACTGTTACCTC 290
Qy 241 GTGGGCTTCAGACACCGCGGGGTGCTGGAGTTCCGGAAGACCGGACACCCAC 300
Db 291 GTGGGCTTCAGACACCGCGGGGTGCTGGAGTTCCGGAAGACCGGACACCCAC 350
Qy 301 CTCCTCGGCGAACAACCCAGTGGCTCGGCTTCGGGCGAGGTACAGGACCTCATCGGC 360
Db 351 CTCCTCGGCGAACAACCCAGTGGCTCGGCTTCGGGCGAGGTACAGGACCTCATCGGC 410
Qy 361 AACAGGCTTCGAGACGCTCAGTACCTAGGCGCGCGGAAATGACAGGCGCTCAACGAC 420
Db 411 AACAGGCTTCGAGACGCTCAGTACCTAGGCGCGCGGAAATGACAGGCGCTCAACGAC 470
Qy 421 CTGGCGAAGAAGAGCGGCTGACCCACAGGCGGACACGAGGAGCTGGTGAAG 480
Db 471 CTGGCGAAGAAGAGCGGCTGACCCACAGGCGGACACGAGGAGCTGGTGAAG 530
Qy 481 CTGGTGGTCATGGTGTGCGAGGGCTGCGGTTCAACACCGTGTCCCGACGTTGACCGG 540
Db 531 CTGGTGGTCATGGTGTGCGAGGGCTGCGGTTCAACACCGTGTCCCGACGTTGACCGG 590
Qy 541 GGGTTCAACAGCAGCAGCGGGTGACTTGACCGTGACGAGGGGAGCAGGTGCGAAG 600
Db 591 GGGTTCAACAGCAGCAGCGGGTGACTTGACCGTGACGAGGGGAGCAGGTGCGAAG 650
Qy 601 TGGGACAGGATCTCCAAAGCGGCTTCGAGTGGGCTGACCCACCGCTGTGATCCCC 660
Db 651 TGGGACAGGATCTCCAAAGCGGCTTCGAGTGGGCTGACCCACCGCTGTGATCCCC 710
Qy 661 GACATCAGAGCTTGGCTCAAGGATAAGAACGAGCAGCAGGATCGTTGCGCTCGTT 720
Db 711 GACATCAGAGCTTGGCTCAAGGATAAGAACGAGCAGCAGGATCGTTGCGCTCGTT 770
Qy 721 AAGAATCAAACTACTGCGCTGCC 744
Db 771 AAGAATCAAACTACTGCGCTGCC 794

RESULT 4

AAQ20478

AAQ20478 standard; DNA; 978 BP.

XX AAQ20478;

AC AAQ20478;

XX AAQ20478;

DT 13-APR-1992 (first entry)

DE Maize RIP deriv. RDT.

XX Ribosome-inactivating protein; alpha RIP; beta RIP; alpha-beta RIP;

KW HIV; tumour; ss.

XX Zea mays.

XX Key Location/Qualifiers

FT CDS 51..815

FT /*tag= a

FT /label= RDT

XX /note= "RIP deriv."

PN BP466222-A.

XX 15-JAN-1992.
PD
XX 10-JUN-1991; 91EP-0201436.
PF
XX 11-JUN-1990; 90US-0535636.
PR
XX (DOWC) DOWELANCO.
PA
XX Walsh TA, Hey TD, Morgan AER;
PI
XX WPI; 1992-017847/03.
DR
P-PSDB; AAR20081.
XX
XX New plant ribosome inactivating proteins and inactive precursors
PT - expressed in eukaryotic cells, useful e.g. in tumour or HIV
PT treatment, and new DNA encoding them
XX
XX Disclosure; Page 25; 40pp; English.
CC The RIP deriv., RDT, encodes a protein (28.233 kD) with a truncated
CC leader, deleted linker and truncated carboxy terminus. It appears
CC to be a more potent inhibitor of protein synthesis than R30-DL
CC (having the linker and leader fragments deleted from proRIP).
CC See also AAQ20476-82.
XX

Sequence 978 BP; 250 A; 271 C; 274 G; 183 T; 0 other;

Query Match 98.8%; Score 740.8; DB 13; Length 978;

Best Local Similarity 99.7%; Pred. No. 6.6e-148;

Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGAAAAGTAAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGGACGCGAACTACCT 60
Db 51 ATGAAAAGTAAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGGACGCGAACTACCT 110
Qy 61 TACAGCGCTTCATCGCTCGTTCGGGAAAGACGTGATCAAAACACTGACACCATATAA 120
Db 111 TACAGCGCTTCATCGCTCGTTCGGGAAAGACGTGATCAAAACACTGACACCATATAA 170
Qy 121 GGGATCTTCAGCGCTTCGTCACCGGAGAAAGGTCCTCGGAGCTATGTTTACACA 180
Db 171 GGGATCTTCAGCGCTTCGTCACCGGAGAAAGGTCCTCGGAGCTATGTTTACACA 230
Qy 181 GAACTCAAACTAGACACGCTCCATCAGCTCGCCATACGATGACAACTGTTACCTC 240
Db 231 GAGCTCAAACTAGACACGCTCCATCAGCTCGCCATACGATGACAACTGTTACCTC 290
Qy 241 GTGGGCTTCAGACACCGCGGGGTGCTGGAGTTCCGGAAGACCGGACACCCAC 300
Db 291 GTGGGCTTCAGACACCGCGGGGTGCTGGAGTTCCGGAAGACCGGACACCCAC 350
Qy 301 CTCCTCGGCGAACAACCCAGTGGCTCGGCTTCGGGCGAGGTACAGGACCTCATCGGC 360
Db 351 CTCCTCGGCGAACAACCCAGTGGCTCGGCTTCGGGCGAGGTACAGGACCTCATCGGC 410
Qy 361 AACAGGCTTCGAGACGCTCAGTACCTAGGCGCGGAAATGACAGGCGCTCAACGAC 420
Db 411 AACAGGCTTCGAGACGCTCAGTACCTAGGCGCGGAAATGACAGGCGCTCAACGAC 470
Qy 421 CTGGCGAAGAAGAGCGGCTGACCCACAGGCGGACACGAGGAGCTGGTGAAG 480
Db 471 CTGGCGAAGAAGAGCGGCTGACCCACAGGCGGACACGAGGAGCTGGTGAAG 530
Qy 481 CTGGTGGTCATGGTGTGCGAGGGCTGCGGTTCAACACCGTGTCCCGACGTTGACCGG 540
Db 531 CTGGTGGTCATGGTGTGCGAGGGCTGCGGTTCAACACCGTGTCCCGACGTTGACCGG 590
Qy 541 GGGTTCAACAGCAGCAGCGGGTGACTTGACCGTGACGAGGGGAGCAGGTGCGAAG 600
Db 591 GGGTTCAACAGCAGCAGCGGGTGACTTGACCGTGACGAGGGGAGCAGGTGCGAAG 650
Qy 601 TGGGACAGGATCTCCAAAGCGGCTTCGAGTGGGCTGACCCACCGCTGTGATCCCC 660

Db 651 TGGGACAGGATCTCCAAAGCGGCTTCGAGTGGGCTGACACCCACCGCTGTGATCCGC 710
QY 661 GACATGCAAGCTTGGCATCAAGGATAGAGACGAGGATCGTTCGGCTCGTT 720
Db 711 GACATGCAAGCTTGGCATCAAGGATAGAGACGAGGATCGTTCGGCTCGTT 770

QY 721 AAGAATCAAACTACTCCCGTGCC 744
Db 771 AAGAATCAAACTACTCCCGTGCC 794

RESULT 5

AAAT79864
ID AAAT79864 standard; DNA; 978 BP.

XX
AC AAAT79864;

DT 25-MAR-2003 (updated)

DT 01-DEC-1997 (first entry)

XX Truncated pro-ribosome inactivating protein gene clone RDT.

XX Maize; proRIP; ribosome inactivating protein; alpha; beta subunit;
XX internal linker; Barley Translation Inhibitor; Trichosanthin;
XX Ricin A-chain; Abrin-A-chain; Saporin; SLT-1; Luffin A; MAP;
XX Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30;
XX therapeutic toxin; tumour cell targeted; protein synthesis inhibitor;
XX post-translational modification; cancer; neoplasia; HIV; AIDS;
XX human immunodeficiency virus; acquired immune deficiency syndrome; ss.

XX Zea mays.

XX Key Location/Qualifiers
XX CDS 51..815
XX /*tag= a

XX US5646026-A.

XX 08-JUL-1997.

XX 07-JUN-1995; 95US-0485286.

XX 09-DEC-1992; 92US-0987927.

XX 11-JUN-1990; 90US-0535636.

XX 26-JAN-1995; 95US-0378761.

XX 07-JUN-1995; 95US-0485286.

XX (DOWC) DOWELANCO.

XX Hey TD, Morgan AER, Walsh TA;

XX WPI: 1997-362934/33.

XX P-PSDB; AAW25126.

XX DNA encoding pro-ribosome inactivating proteins - inactive
XX precursors of ribosome inactivating proteins; can be expressed in
XX eukaryotic cells without causing cell death

XX Claim 2; Column 51-52; 186pp; English.

XX AAAT79864 encodes a single chain maize pro-ribosome inactivating protein
XX (proRIP) having a truncated leader sequence and carboxy terminus
XX engineered for expression in Escherichia coli.
XX The sequence contains no linker separating the alpha and beta subunit
XX regions and was shown to be a potent inhibitor of protein synthesis.
XX proRIP sequences can be engineered to contain a selectively removable
XX internal peptide linker sequence separating the alpha and beta units
XX of the RIP protein to form an inactive form of RIP. When separated
XX the two units regain activity and are capable of inactivating eukaryotic
XX ribosomes and hence preventing protein production. Many different
XX Panacoidae RIPs may be produced with an internal linker including:
XX Barley Translation Inhibitor, Trichosanthin, Ricin A-chain, Abrin-A

CC A-chain, Saporin, SLT-1, Luffin A, MAP, Ricinus communis agglutinin,
CC Momordin, PAP-S, Luffin-B and Dianthin 30. The RIPs can be used in
CC the construction of therapeutic toxins targeted to specific cells such
CC as tumour cells via the attachment of a targeting polypeptide, e.g. a
CC monoclonal antibody. A further use is in HIV therapy (see US4869903).
CC There is interest in expressing RIP recombinantly in host eukaryotic
CC cells, because of the capacity to provide correct post-translational
CC processing. However, RIPs effectively inhibit protein synthesis in
CC eukaryotic cells resulting in cell death. Since the proRIP proteins
CC are not cytotoxic to eukaryotic cells, they can be recombinantly
CC expressed in such cells and then converted to active RIP proteins.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
XX

XX Sequence 978 BP; 250 A; 271 C; 275 G; 182 T; 0 other;

XX Query Match 98.8%; Score 740.8; DB 18; Length 978;

XX Best Local Similarity 99.7%; Pred. No. 6.6e-148; Indels 0; Gaps 0;

XX Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAAGAAATAGTGCCTAAAGTTCACTGAAATCTTCCCGTGGAGACGCGAATACCT 60

Db 51 ATGAAAGAAATAGTGCCTAAAGTTCACTGAAATCTTCCCGTGGAGACGCGAATACCT 110

QY 61 TACAGGCGCTTCATCGCTGCTCGGAAAGAGTGCATCAAACTGACCCACCAATAA 120

Db 111 TACAGGCGCTTCATCGCTGCTCGGAAAGAGTGCATCAAACTGACCCACCAATAA 170

QY 121 GGGATCTTCCAGCGCTGCTGCCACCGGAGAGAGTCCCGGAGCTATGTTTACACA 180

Db 171 GGGATCTTCCAGCGCTGCTGCCACCGGAGAGAGTCCCGGAGCTATGTTTACACA 230

QY 181 GAACTGAAATAGGACCAAGTCCATCAGCTCGCCATACGATGACAACTGTACCTC 240

Db 231 GAGCTCAAAATAGGACCAAGTCCATCAGCTCGCCATACGATGACAACTGTACCTC 290

QY 241 GTGGGCTTCAGGACCCCGGCGGGTGTGGTGGAGTTCGGCAAGACGGCGACACCCAC 300

Db 291 GTGGGCTTCAGGACCCCGGCGGGTGTGGTGGAGTTCGGCAAGACGGCGACACCCAC 350

QY 301 CTCCTCGGCGACAAACCCAGAGTGGTTCGGCTTCGGCGGAGGTACCCAGACCTCATCGGC 360

Db 351 CTCCTCGGCGACAAACCCAGAGTGGTTCGGCTTCGGCGGAGGTACCCAGACCTCATCGGC 410

QY 361 AACAAAGGCTTCGGAGACCGTCCATATGGCCCGCGCGAATGACAGGCGCGTCAACGAC 420

Db 411 AACAAAGGCTTCGGAGACCGTCCATATGGCCCGCGCGAATGACAGGCGCGTCAACGAC 470

QY 421 CTGGCGAAGAAAGAGGCGGCTGACCCACAGGCGGACACGAGAGCAAGCTGTGAAG 480

Db 471 CTGGCGAAGAAAGAGGCGGCTGACCCACAGGCGGACACGAGAGCAAGCTGTGAAG 530

QY 481 CTGGTGTTCATGTGTGCGAGGGGCTGCGGTTCAACACCGTGTCCCGCACGGTGGACGG 540

Db 531 CTGGTGTTCATGTGTGCGAGGGGCTGCGGTTCAACACCGTGTCCCGCACGGTGGACGG 590

QY 541 GGGTTCAACAGCCAGCACCGGCTGACCTTGAACGTTGACCGAGGAGGAGGAGTGCAGAG 600

Db 591 GGGTTCAACAGCCAGCACCGGCTGACCTTGAACGTTGACCGAGGAGGAGGAGTGCAGAG 650

QY 601 TGGGACAGGATCTCCAAAGCGGCTTCGAGTGGGCTGACACCCACCGCTGTGATCCCC 660

Db 651 TGGGACAGGATCTCCAAAGCGGCTTCGAGTGGGCTGACACCCACCGCTGTGATCCCC 710

QY 661 GACATGCAAGCTTGGCATCAAGGATAGAGACGAGGATCGTTCGGCTCGTT 720

Db 711 GACATGCAAGCTTGGCATCAAGGATAGAGACGAGGATCGTTCGGCTCGTT 770

QY 721 AAGAATCAAACTACTCCCGTGCC 744

Db 771 AAGAATCAAACTACTCCCGTGCC 794

RESULT 6

XX 09-DEC-1992; 92US-0987927.
 PR 11-JUN-1990; 90US-0535636.
 PR 26-JAN-1995; 95US-0378761.
 PR 07-JUN-1995; 95US-0485286.
 XX (DOWC) DOWELANCO.
 PA Hey TD, Morgan AER, Walsh TA;
 XX WPI; 1997-362934/33.
 XX P-PSDB; AAW25125.
 XX DNA encoding pro-ribosome inactivating proteins - inactive
 PT precursors of ribosome inactivating proteins; can be expressed in
 PT eukaryotic cells without causing cell death
 XX Claim 2; Column 47-50; 186pp; English.
 XX Claim 279863 encodes a single chain maize pro-ribosome inactivating protein
 CC (proRIP) with no leader sequence and no linker separating the alpha
 CC and beta units. proRIP sequences can be engineered to contain a
 CC selectively removable internal peptide linker sequence separating the
 CC alpha and beta units of the RIP protein to form an inactive form of RIP.
 CC When separated the two units regain activity and are capable of
 CC inactivating eukaryotic ribosomes and hence preventing protein
 CC production. Many different Panicoideae RIPs may be produced with an
 CC internal linker including: Barley Translation Inhibitor, Trichosanthin,
 CC Ricin A-chain, Abrin-A A-chain, Saporin, SLT-1, Luffin A, MAP, Ricinus
 CC communis agglutinin, Momordin, PAP-S, Luffin-B and Dianthin 30. The RIPs
 CC can be used in the construction of therapeutic toxins targeted to
 CC specific cells such as tumour cells via the attachment of a targeting
 CC polypeptide, e.g. a monoclonal antibody. A further use is in HIV therapy
 CC (see US4869903). There is interest in expressing RIP recombinantly in
 CC host eukaryotic cells, because of the capacity to provide correct
 CC post-translational processing. However, RIPs effectively inhibit protein
 CC synthesis in eukaryotic cells resulting in cell death. Since the proRIP
 CC proteins are not cytotoxic to eukaryotic cells, they can be
 CC recombinantly expressed in such cells and then converted to active RIP
 CC proteins.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX Sequence 984 BP; 255 A; 270 C; 279 G; 180 T; 0 other;
 SQ Query Match 98.8%; Score 740.8; DB 18; Length 984;
 Best Local Similarity 99.7%; Pred. No. 6.6e-148;
 Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ATGAAAGAATAGTGCCTAAAGTTTCACTGAAATCTTCCCGTGGAGACGGAACCTACCTT 60
 DB |||||
 QY 37 ATGAAAGAATAGTGCCTAAAGTTTCACTGAAATCTTCCCGTGGAGACGGAACCTACCTT 96
 DB |||||
 QY 61 TACAGCGCTTTCATCCGTCGGTCCGGAAGAGCTGATCAAAACACATGCACCGACCATATAA 120
 DB |||||
 QY 97 TACAGCGCTTTCATCCGTCGGTCCGGAAGAGCTGATCAAAACATGCACCGACCATATAA 156
 DB |||||
 QY 121 GGGATCTTCCAGCCCGTGTGTCACCGAGAGAGGTCCCGGAGCTATGTTTTCACACA 180
 DB |||||
 QY 157 GGGATCTTCCAGCCCGTGTGTCACCGAGAGAGGTCCCGGAGCTATGTTTTCACACA 216
 DB |||||
 QY 181 GAACTGAAACTAGGACCGAGCTCCATCAGCTGCCATACGATCGATGACAACTGTACCTC 240
 DB |||||
 QY 217 GAGCTCAAAACTAGGACCGAGCTCCATCAGCTGCCATACGATGACAACTGTACCTC 276
 DB |||||
 QY 241 GTGGGCTTCAGGACCCCGGGCGGGGTGTGGAGTTCGGCAAGACGCGGACACCCAC 300
 DB |||||
 QY 277 GTGGGCTTCAGGACCCCGGGCGGGGTGTGGAGTTCGGCAAGACGCGGACACCCAC 336
 DB |||||
 QY 301 CTCCTCGGCGAACACCCCGAGTGGCTCGGCTTCGGGGCGGAGGTACAGGACCTCATCGGC 360
 DB |||||
 QY 337 CTCCTCGGCGAACACCCCGAGTGGCTCGGCTTCGGGGCGGAGGTACAGGACCTCATCGGC 396
 DB |||||
 QY 361 AACAGGGTCTGGAGACCGTCAACCATGGGCCCGCGGCAAAATGACAGGCGCGTCAACGAC 420

DB |||||
 QY 397 AACAGGGTCTGGAGACCGTCAACCATGGCGCGCGGAAATGACCAAGGCGCGTCAACGAC 456
 DB |||||
 QY 421 CTGGCGAAGAAAGAGCGCGCTACCCACAGGCGCGACACCAAGAGCAAGCTGGTGAG 480
 DB |||||
 QY 457 CTGGCGAAGAAAGAGCGCGCTACCCACAGGCGCGACACCAAGAGCAAGCTGGTGAG 516
 DB |||||
 QY 481 CTGGTGGTTCATGGTGTGGAGGGGTGCGGTTTCAACACCGTTCGCCGACCGTGGACGCG 540
 DB |||||
 QY 517 CTGGTGGTTCATGGTGTGGAGGGGTGCGGTTTCAACACCGTTCGCCGACCGTGGACGCG 576
 QY 541 GGGTTCAACAGCCAGCAGCGGGGTGACCTTGACCGGTGACGCGAGGGAAGCAGGTGCAGAA 600
 DB 577 GGGTTCAACAGCCAGCAGCGGGGTGACCTTGACCGGTGACGCGAGGGAAGCAGGTGCAGAA 636
 QY 601 TGGGACAGGATCTCCAAGCGCGCTTCGAGTGGGTGACCAACCGCTGTGATCCCC 660
 DB |||||
 QY 637 TGGGACAGGATCTCCAAGCGCGCTTCGAGTGGGTGACCAACCGCTGTGATCCCC 696
 QY 661 GACATGCAAGACTTGGGATCAAGGATAAGAAACGAGGAGGATCGTTGCGCTCGTT 720
 DB 697 GACATGCAAGACTTGGGATCAAGGATAAGAAACGAGGAGGATCGTTGCGCTCGTT 756
 QY 721 AAGAATCAAACTACTGCGCGTCCC 744
 DB |||||
 QY 757 AAGAATCAAACTACTGCGCGTCCC 780
 XX RESULT 8
 XX AAT77755
 XX ID AAT77755 standard; DNA; 985 BP.
 XX AC AAT77755;
 XX DT 25-MAR-2003 (updated)
 XX DT 26-SEP-1997 (first entry)
 XX DE RIP fusion protein, R30-DL coding sequence.
 XX KW pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer;
 KW inactivation; eukaryotic ribosome; alpha fragment; beta fragment;
 KW inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver;
 KW rat; ribosomal 28S RNA; cellular proliferation; HIV-infected T cell; ss.
 XX OS Synthetic.
 XX Key Location/Qualifiers
 XX CDS 37..822
 XX FT /*tag= a
 XX FT /product= R30-DL
 XX PN US5635384-A.
 XX PD 03-JUN-1997.
 XX PF 26-JAN-1995; 95US-0378761.
 XX PR 09-DEC-1992; 92US-0987927.
 XX PR 11-JUN-1990; 90US-0535636.
 XX PR 26-JAN-1995; 95US-0378761.
 XX PA (DOWC) DOWELANCO.
 XX PI Hey TD, Morgan AER, Walsh TA;
 XX DR WPI; 1997-309831/28.
 XX DR P-PSDB; AAW21712.
 XX Inactive precursor of maize ribosome-inactivating protein - also
 PT chimeric ribosome-inactivating protein precursors containing
 PT internal linker sequences
 XX Claim 4; Column 45-48; 121pp; English.

XX CC The sequences given in AAT7754-63 encode fusion proteins which are
CC examples of Ribosome Inactivating Proteins. RIPS are potent inhibitors
CC of eukaryotic protein synthesis. They possess a highly specific
CC N-glycosidase activity which cleaves the glycosidic bond of adenine
CC 4324 of rat liver ribosomal 28S RNA. RIPs selectively inhibit
CC cellular proliferation of cells, e.g. cancer cells and HIV-infected
CC T cells. The inactive proRIP proteins make it possible to provide
CC protein synthesis inhibitors with uses in practical and improved
CC ways not before possible. The RIP can be used to make cytotoxic
CC conjugates.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX SQ Sequence 985 BP; 255 A; 271 C; 279 G; 180 T; 0 other;
Query Match 98.8%; Score 740.8; DB 18; Length 985;
Best Local Similarity 99.7%; Pred. No. 6.6e-148; Indels 0; Gaps 0;
Matches 742; Conservative 0; Mismatches 2;
QY 1 ATGAAAGAAATAGTGCACAAAGTTCACTGAAATCTTCCCGTGAGGACGCGAACTACCCCT 60
Db |||||
QY 37 ATGAAAGAAATAGTGCACAAAGTTCACTGAAATCTTCCCGTGAGGACGCGAACTACCCCT 96
Db |||||
QY 61 TAGAGCGCTTCATCGGTGGTCCGGAAGAGTGATCAACACATGTCACCGACCATATAA 120
Db |||||
QY 97 TAGAGCGCTTCATCGGTGGTCCGGAAGAGTGATCAACACATGTCACCGACCATATAA 156
Db |||||
QY 121 GGGATCTTCCAGCCCGTGTGCCACCGAGAGAGGTGCCGGAGCTATGTTCTACACA 180
Db |||||
QY 157 GGGATCTTCCAGCCCGTGTGCCACCGAGAGAGGTGCCGGAGCTATGTTCTACACA 216
Db |||||
QY 181 GATCTGAAATCTAGGACCACTCAATCACTGCCATACGATGGAACACCTGTACCTC 240
Db |||||
QY 217 GAGCTCAAAATAGGACCACTCAATCACTGCCATACGATGGAACACCTGTACCTC 276
Db |||||
QY 241 GTGGCTTTCAGGACCCCGGGGGTGTGGTGGAGTTCGGCAAGAGCGGACCCAC 300
Db |||||
QY 277 GTGGCTTTCAGGACCCCGGGGGTGTGGTGGAGTTCGGCAAGAGCGGACCCAC 336
Db |||||
QY 301 CTCCTCGGACACACCCAGGTGGCTCGGCTTCGGCGGAGGTACAGGACCTCATCGGC 360
Db |||||
QY 337 CTCTCGGACACACCCAGGTGGCTCGGCTTCGGCGGAGGTACAGGACCTCATCGGC 396
Db |||||
QY 361 AACAGGCTTGAGACCGGTCAACATGGCGCGGCCGAAATGACCGGCGGTCAAGCAC 420
Db |||||
QY 397 AACAGGCTTGAGACCGGTCAACATGGCGCGGCCGAAATGACCGGCGGTCAAGCAC 456
Db |||||
QY 421 CTGCGAAGAGAGAGGCGGCTGACCCACAGCGCGACAGAGAGAGCTGTGAAG 480
Db |||||
QY 457 CTGCGAAGAGAGAGGCGGCTGACCCACAGCGCGACAGAGAGAGCTGTGAAG 516
Db |||||
QY 481 CTGCTGTCTATGTTGTCGAGGGGCTCGGCTTCAACACCGCTGCCCGAGCGGAGCGG 540
Db |||||
QY 517 CTGCTGTCTATGTTGTCGAGGGGCTCGGCTTCAACACCGCTGCCCGAGCGGAGCGG 576
Db |||||
QY 541 GGGTTCAACGACGACGCGGGGTGACCTTGACCGTGAACGAGGGAAGCGAGGTGCAGAG 600
Db |||||
QY 577 GGGTTCAACGACGACGCGGGGTGACCTTGACCGTGAACGAGGGAAGCGAGGTGCAGAG 636
Db |||||
QY 601 TGGGACAGGATCTCCAGGCGGCTTCAGTGGCTGACACCCACCCCGCTGTGATCCCC 660
Db |||||
QY 637 TGGGACAGGATCTCCAGGCGGCTTCAGTGGCTGACACCCACCCCGCTGTGATCCCC 696
Db |||||
QY 661 GACATGACAGGCTTGGCATCAAGGATAAGAAAGACGAGGATCGTTGGCGCTCGTT 720
Db |||||
QY 697 GACATGACAGGCTTGGCATCAAGGATAAGAAAGACGAGGATCGTTGGCGCTCGTT 756
Db |||||
QY 721 AAGATCAAACTACTGCGGTGCC 744
Db |||||
QY 757 AAGATCAAACTACTGCGGTGCC 780
Db |||||

RESULT 9

AAT79866
ID AAT79866 standard; DNA; 1161 BP.
XX AC AAT79866;
XX AC AAT79866;
DT 25-MAR-2003 (updated)
DT 01-DEC-1997 (first entry)
DE Pro-ribosome inactivating protein gene clone RDT-A.
XX Maize; proRIP; ribosome inactivating protein; alpha; beta subunit;
XX internal linker; Barley translation inhibitor; Trichosanthin;
XX Ricin A-chain; Abrin-A chain; Saporin; PAP-S; Luffin A; MAP;
XX Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30;
XX therapeutic toxin; tumour cell targeted; protein synthesis inhibitor;
XX post-translational modification; cancer; neoplasia; HIV; AIDS;
XX human immunodeficiency virus; acquired immune deficiency syndrome; ss.
OS Zea mays.
XX Key Location/Qualifiers
XX CDS 51..998
XX /*tag= a
XX US5646026-A.
XX 08-JUL-1997.
XX 07-JUN-1995; 95US-0485286.
XX 09-DEC-1992; 92US-0987927.
XX 11-JUN-1990; 90US-0535636.
XX 26-JAN-1995; 95US-0378761.
XX 07-JUN-1995; 95US-0485286.
XX (DOWC) DOWELANCO.
XX Hey TD, Morgan ABR, Walsh TA;
XX WPI; 1997-362934/33.
XX P-PSDB; AAW25128.
XX DNA encoding pro-ribosome inactivating proteins - inactive
XX precursors of ribosome inactivating proteins; can be expressed in
XX eukaryotic cells without causing cell death
XX Claim 2; Column 57-60; 186pp; English.
XX AAT79866 encodes a single chain maize pro-ribosome inactivating protein
XX (proRIP) having a truncated leader sequence and carboxy terminus
XX engineered for expression in Escherichia coli and which binds to
XX immunoglobulin IgG. The construct has a sequence encoding the single
XX antibody binding region (ABR) domain from Staphylococcus aureus antibody
XX binding protein A (ABR-A) inserted into a BamHI site. The sequence
XX contains no linker separating the alpha and beta subunit regions and
XX was shown to be a potent inhibitor of protein synthesis and bound
XX specifically to IgG.
XX proRIP sequences can be engineered to contain a selectively removable
XX internal peptide linker sequence separating the alpha and beta units
XX of the RIP protein to form an inactive form of RIP. When separated
XX the two units regain activity and are capable of inactivating eukaryotic
XX ribosomes and hence preventing protein production. Many different
XX Panacoidae RIPS may be produced with an internal linker including:
XX Barley translation inhibitor, Trichosanthin, Ricin A-chain, Abrin-A
XX A-chain, Saporin, SLT-1, Luffin A, MAP, Ricinus communis agglutinin,
XX Momordin, PAP-S, Luffin-B and Dianthin 30. The RIPS can be used in
XX the construction of therapeutic toxins targeted to specific cells such
XX as tumour cells via the attachment of a targeting polypeptide, e.g. a
XX monoclonal antibody. A further use is in HIV therapy (see US4869903).
XX There is interest in expressing RIP recombinantly in host eukaryotic
XX cells, because of the capacity to provide correct post-translational
XX processing. However, RIPS effectively inhibit protein synthesis in
XX eukaryotic cells resulting in cell death. Since the proRIP proteins

QY 301 CTCCTCGGCGACACCCAGTGGCTTGGCTTGGCGGCGAGTACCGAGCTCATCGGC 360
 Db |||||
 QY 351 CTCCTCGGCGACACCCAGTGGCTTGGCTTGGCGGCGAGTACCGAGCTCATCGGC 410
 Db |||||
 QY 361 AACAAAGGCTCTGGAGACCGTCAACATGGCGCGCGGAAATGACACAGGCGCTCAACGAC 420
 Db |||||
 QY 411 AACNAGGCTCTGGAGACCGTCAACATGGCGCGCGGAAATGACACAGGCGCTCAACGAC 470
 Db |||||
 QY 421 CTGCGGAAGAAGAAAGGCGGCTGACCCACAGCGCCGACACGAAAGACGCTCGTGAAG 480
 Db |||||
 QY 471 CTGCGGAAGAAGAAAGGCGGCTGACCCACAGCGCCGACACGAAAGACGCTCGTGAAG 530
 Db |||||
 QY 481 CTGCTGCTCATGCTGTCGAGGGGCTCGGTTCAACACCGTGTCCCGACGCTGGAGCGG 540
 Db |||||
 QY 531 CTGCTGCTCATGCTGTCGAGGGGCTCGGTTCAACACCGTGTCCCGACGCTGGAGCGG 590
 Db |||||
 QY 541 GGGTTCAACAGCCAGCAGCGGCTGACCTTGACCGTGAACGAGGGGAGCAGGTGCAGAG 600
 Db |||||
 QY 591 GGGTTCAACAGCCAGCAGCGGCTGACCTTGACCGTGAACGAGGGGAGCAGGTGCAGAG 650
 Db |||||
 QY 601 TGGGACAGGATCTCAAGCGGCTTCGAGTGGGCTGACCAACCCCGCTGTGATCCCC 660
 Db |||||
 QY 651 TGGGACAGGATCTCAAGCGGCTTCGAGTGGGCTGACCAACCCCGCTGTGATCCCC 710
 Db |||||
 QY 661 GACATCAGAGCTTGGCATCAGGATAAGAAAGAGCAGGAGTCTGTCGCTCGTT 720
 Db |||||
 QY 711 GACATCAGAGCTTGGCATCAGGATAAGAAAGAGCAGGAGTCTGTCGCTCGTT 770
 Db |||||
 QY 721 AAGAATCAAACTACTGCGCGTGC 744
 Db |||||
 QY 771 AAGAATCAAACTACTGCGCGTGC 794
 Db |||||

RESULT 11

AAT79867

ID AAT79867 standard; DNA; 1422 BP.

AC AAT79867;

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WPI; 1997-362934/33.
 P-PSDB; AAW25129.
 DNA encoding pro-ribosome inactivating proteins - inactive precursors of ribosome inactivating proteins; can be expressed in eukaryotic cells without causing cell death
 Claim 2; Column 61-66; 186pp; English.
 AAT79867 encodes a single chain maize pro-ribosome inactivating protein (proRIP) having a truncated leader sequence and carboxy terminus engineered for expression in *Escherichia coli* and which binds to immunoglobulin IGG. The construct has a sequence encoding the single antibody binding region (ABR) domains from *Staphylococcus aureus* antibody binding Protein A (ABR-A) and *Streptococcus* Group G protein G (ABR-G) inserted into a BamHI site. The sequence contains no linker separating the alpha and beta subunit regions and was shown to be a potent inhibitor of protein synthesis and bound specifically to IGG.
 proRIP sequences can be engineered to contain a selectively removable internal peptide linker sequence separating the alpha and beta units of the RIP protein to form an inactive form of RIP. When separated the two units regain activity and are capable of inactivating eukaryotic ribosomes and hence preventing protein production. Many different Panacoidae RIPs may be produced with an internal linker including: Barley Translation Inhibitor, Trichosanthin, Ricin A-chain, Abrin-A A-chain, Saporin, SLT-1, Luffin A, MAP, Ricinus communis agglutinin, Momordin, PAP-S, Luffin-B and Dianthin 30. The RIPs can be used in the construction of therapeutic toxins targeted to specific cells such as tumour cells via the attachment of a targeting polypeptide, e.g. a monoclonal antibody. A further use is in HIV therapy (see US4869903). There is interest in expressing RIP recombinantly in host eukaryotic cells, because of the capacity to provide correct post-translational processing. However, RIPs effectively inhibit protein synthesis in eukaryotic cells resulting in cell death. Since the proRIP proteins are not cytotoxic to eukaryotic cells, they can be recombinantly expressed in such cells and then converted to active RIP proteins.
 (Updated on 25-MAR-2003 to correct PF field.)

SQ Sequence 1422 BP; 420 A; 364 C; 357 G; 281 T; 0 other;

Query Match 98.8%; Score 740.8; DB 18; Length 1422;
 Best Local Similarity 99.7%; Pred. No. 6.9e-148;
 Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAAGAAATAGTCCAAAGTTCATGAAATCTCCCGTGAGAGACCGCACTACCT 60
 Db |||||
 QY 51 ATGAAAGAAATAGTCCAAAGTTCATGAAATCTCCCGTGAGAGACCGCACTACCT 110
 Db |||||
 QY 61 TACAGCGCTTCATCGCGTCCGGAAGACGTGATCAAACTGCAACCGACCATAA 120
 Db |||||
 QY 111 TACAGCGCTTCATCGCGTCCGGAAGACGTGATCAAACTGCAACCGACCATAA 170
 Db |||||
 QY 121 GGGATCTTCAGCGCTGCTGCCACCGAGAAAGAGTCCCGAGCTATGTTTACACA 180
 Db |||||
 QY 171 GGGATCTTCAGCGCTGCTGCCACCGAGAAAGAGTCCCGAGCTATGTTTACACA 230
 Db |||||
 QY 181 GAACTGAAACTAGAACGAGCTCCATCAGCTCGGCATACGATCGACAACTGTTACCTC 240
 Db |||||
 QY 231 GAGCTCAAACTAGAACGAGCTCCATCAGCTCGGCATACGATCGACAACTGTTACCTC 290
 Db |||||
 QY 241 GTGGCTTCAGGACCCCGGGGGGTGTGGTGGAGTTCGGCAGGACGGGACACCCAC 300
 Db |||||
 QY 291 GTGGCTTCAGGACCCCGGGGGGTGTGGTGGAGTTCGGCAGGACGGGACACCCAC 350
 Db |||||
 QY 301 CTCTCGGCGACAAACCCAGGTGGCTCGGCTTCGGCGGAGGTACACAGGACCTATCGGC 360
 Db |||||
 QY 351 CTCTCGGCGACAAACCCAGGTGGCTCGGCTTCGGCGGAGGTACACAGGACCTATCGGC 410
 Db |||||
 QY 361 AACAGGGCTCTGGAGACCGTCAACATGGCGCGCGGAAATGACACAGGCGCTCAACGAC 420
 Db |||||
 QY 411 AACAGGGCTCTGGAGACCGTCAACATGGCGCGCGGAAATGACACAGGCGCTCAACGAC 470
 Db |||||

Pro-ribosome inactivating protein gene clone RDT-G-A.

Maize; proRIP; ribosome inactivating protein; alpha; beta subunit;
 internal linker; Barley Translation Inhibitor; Trichosanthin;
 Ricin A-chain; Abrin-A A-chain; Saporin; SLT-1; Luffin A; MAP;
 Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30;
 therapeutic toxin; tumour cell targeted; protein synthesis inhibitor;
 post-translational modification; cancer; neoplasia; HIV; AIDS;
 human immunodeficiency virus; acquired immune deficiency syndrome; ss.

Zea mays.

Key Location/Qualifiers

FH 51.1259

CDS /*tag= a

US5646026-A.

PD 08-JUL-1997.

XX

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QY 421 CTGCGAAGAAAGAGAGGGGGCTGACCCACAGCCGACACGAGAGCAAGCTGGTGAAG 480
 DB 471 CTGCGAAGAAAGAGAGGGGGCTGACCCACAGCCGACACGAGAGCAAGCTGGTGAAG 530
 QY 481 CTGCTGTCTATGGTGTGCGAGGGGCTGGGTTCAACACCGTGTCCCGACGGTGGACGG 540
 DB 531 CTGCTGTCTATGGTGTGCGAGGGGCTGGGTTCAACACCGTGTCCCGACGGTGGACGG 590
 QY 541 GGGTTCAACAGCCAGCAGCGGGGTGACCTTGACCGTGACGAGGGGAGCAGGTGCGAAG 600
 DB 591 GGGTTCAACAGCCAGCAGCGGGGTGACCTTGACCGTGACGAGGGGAGCAGGTGCGAAG 650
 QY 601 TGGACAGGATCTCCAGGGGGCTTTCAGTGGGCTGACACCCACCGCTGTGATCCCC 660
 DB 651 TGGACAGGATCTCCAGGGGGCTTTCAGTGGGCTGACACCCACCGCTGTGATCCCC 710
 QY 661 GACATGCAAGAGCTTGGCATCAAGGATAAGAAACGAGCAGGAGTCTGTCGCTCGTT 720
 DB 711 GACATGCAAGAGCTTGGCATCAAGGATAAGAAACGAGCAGGAGTCTGTCGCTCGTT 770
 QY 721 AAGAAATCAAACTACTGCGGCTGCC 744
 DB 771 AAGAAATCAAACTACTGCGGCTGCC 794

RESULT 12

AAT77759
 ID AAT77759 standard; DNA; 1422 BP.

AC AAT77759;

DT 25-MAR-2003 (updated)

DT 26-SEP-1997 (first entry)

DE RIP fusion protein, RDT-G-A coding sequence.

OS pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer;
 KW inactivation; eukaryotic ribosome; alpha fragment; beta fragment;
 KW inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver;
 KW rat; ribosomal 28S RNA; cellular proliferation; HIV-infected T cell; ss.

XX Synthetic.

Key Location/Qualifiers
 FT 51..1256
 FT CDS /*tag= a
 FT /product= RDT-G-A

XX US5635384-A.

XX 03-JUN-1997.

XX 26-JAN-1995; 95US-0378761.

XX 09-DEC-1992; 92US-0987927.

XX 11-JUN-1990; 90US-0535636.

XX 26-JAN-1995; 95US-0378761.

XX (DOWC) DOWELANCO.

XX Hey TD, Morgan AER, Walsh TA;

XX WPI; 1997-309831/28.

XX P-PSDB; AAW21716.

XX Inactive precursor of maize ribosome-inactivating protein - also
 PT chimeric ribosome-inactivating protein precursors containing
 PT internal linker sequences

XX Claim 4; Column 61-64; 121pp; English.

XX The sequences given in AAT77754-63 encode fusion proteins which are

CC examples of Ribosome Inactivating Proteins. RIPs are potent inhibitors
 CC of eukaryotic protein synthesis. They possess a highly specific
 CC N-glycosidase activity which cleaves the glycosidic bond of adenine
 CC 4324 of rat liver ribosomal 28S RNA. RIP's selectively inhibit
 CC cellular proliferation of cells, e.g. cancer cells and HIV-infected
 CC T cells. The inactive proRIP proteins make it possible to provide
 CC protein synthesis inhibitors with uses in practical and improved
 CC ways not before possible. The RIP can be used to make cytotoxic
 CC conjugates.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 1422 BP; 420 A; 364 C; 357 G; 281 T; 0 other;

Query Match 98.8%; Score 740.8; DB 18; Length 1422;

Best Local Similarity 99.7%; Pred. No. 6.9e-148;

Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAAGAAATAGTCCCAAGTTCACTGAATCTTCCCGTGGAGGACCGAACTACCCCT 60
 DB 51 ATGAAAGAAATAGTCCCAAGTTCACTGAATCTTCCCGTGGAGGACCGAACTACCCCT 110
 QY 61 TACAGCGCTTCATCGCTCGGTCCGGAAGACGTGATCAAACTGACCGACGACATAAA 120
 DB 111 TACAGCGCTTCATCGCTCGGTCCGGAAGACGTGATCAAACTGACCGACGACATAAA 170
 QY 121 GGGATCTTCCAGCCCGTCTGCCACCGAGAGAGGTCCCGGAGCTATGTTCTACACA 180
 DB 171 GGGATCTTCCAGCCCGTCTGCCACCGAGAGAGGTCCCGGAGCTATGTTCTACACA 230
 QY 181 GAACTGAAATAGGACCAAGTCCATCAGCTTCGCTATACATGGAACAACTGTACTCTC 240
 DB 231 GAGCTCAAAATAGGACCAAGTCCATCAGCTTCGCTATACATGGAACAACTGTACTCTC 290
 QY 241 GTGGCTTCAGACCCCGGGGGGTGTGGTGGAGTTTCGCAAGAGGCGGACACCCAC 300
 DB 291 GTGGCTTCAGACCCCGGGGGGTGTGGTGGAGTTTCGCAAGAGGCGGACACCCAC 350
 QY 301 CTCCTCGGCGACAACCCAGGTGGCTCGGCTTCGGCGGCGAGTACCGAGCTCATCGGC 360
 DB 351 CTCCTCGGCGACAACCCAGGTGGCTCGGCTTCGGCGGCGAGTACCGAGCTCATCGGC 410
 QY 361 AACAGGGTCTGGAGACCGTACCATGGGCGCGCGGAAATGACAGGCGCGTCAACGAC 420
 DB 411 AACAGGGTCTGGAGACCGTACCATGGGCGCGCGGAAATGACAGGCGCGTCAACGAC 470
 QY 421 CTGGCGAAGAGAAAGAGCGGCTGACCCACAGGCGCGACACGAGCAAGCTGTGAAG 480
 DB 471 CTGGCGAAGAGAAAGAGCGGCTGACCCACAGGCGCGACACGAGCAAGCTGTGAAG 530
 QY 481 CTGGTGGTTCATGGTGTGGAGGGGTGCGGTTCAACACCGTGTCCCGACGGTGACGCG 540
 DB 531 CTGGTGGTTCATGGTGTGGAGGGGTGCGGTTCAACACCGTGTCCCGACGGTGACGCG 590
 QY 541 GGGTTCAACAGCCAGCAGCGGGGTGACCTTGACCGTGACGAGGGAAGCAGGTGCGAAG 600
 DB 591 GGGTTCAACAGCCAGCAGCGGGGTGACCTTGACCGTGACGAGGGAAGCAGGTGCGAAG 650
 QY 601 TGGGACAGGATCTCCAAGCGGCGCTTCGAGTGGGTGACACCCCGACCGCTGTGATCCCC 660
 DB 651 TGGGACAGGATCTCCAAGCGGCGCTTCGAGTGGGTGACACCCCGACCGCTGTGATCCCC 710
 QY 661 GACATGCAAGAGCTTGGCATCAAGGATAAGAAACGAGCAGGAGTCTGTCGCTCGTT 720
 DB 711 GACATGCAAGAGCTTGGCATCAAGGATAAGAAACGAGCAGGAGTCTGTCGCTCGTT 770
 QY 721 AAGAAATCAAACTACTGCGGCTGCC 744
 DB 771 AAGAAATCAAACTACTGCGGCTGCC 794

RESULT 13

AAQ20482

ID AAQ20482 standard; DNA; 1683 BP.

XX AAQ20482;
 AC
 XX
 DT 13-APR-1992 (first entry)
 XX
 DE Maize RIP deriv. RDT-G-G-A.
 XX
 KW Ribosome-inactivating protein; alpha RIP; beta RIP; alpha-beta RIP;
 KW HIV; tumour; IGG; immunoglobulin; protein G;
 KW antibody binding domain; ABR; ss.
 XX
 OS Zea mays.
 XX
 FH Key Location/Qualifiers
 FT CDS 51..1520
 FT /*tag= a
 FT /label= RDT-G-G-A
 FT /note= "RIP deriv."
 XX
 XX EP466222-A.
 PN
 XX
 XX 15-JAN-1992.
 PD
 XX
 XX 10-JUN-1991; 91EP-0201436.
 PF
 XX
 XX 11-JUN-1990; 90US-0535636.
 PR
 XX
 XX (DOWC) DOWELANCO.
 PA
 XX
 PI Walsh TA, Hey TD, Morgan AER;
 XX
 DR WPI; 1992-017847/03.
 DR P-PSDB; AAR20085.
 XX
 XX New plant ribosome inactivating proteins and inactive precursors
 PT - expressed in eukaryotic cells, useful e.g. in tumour or HIV
 PT treatment, and new DNA encoding them
 PT
 XX Disclosure; Page 32-33; 40pp; English.
 XX
 XX To increase to binding ability of the RDT-A (AAQ20480) to IgG
 CC antibody binding domain from Streptococcal group G protein G
 CC (ABR-G) was synthesised using oligonucleotides. The ABR-G fragment
 CC was inserted into the BamHI site of RDT-A. Two classes of clones
 CC have been studied. RDT-G-A contains a single ABR-G domain inserted
 CC in the correct orientation between the 3' end of RDT and the 5' end
 CC of ABR-A (AAQ20481). A second class contains two properly oriented
 CC ABR-G domains (AAQ20482).
 CC See also AAQ20476-82.
 XX
 XX Sequence 1683 BP; 513 A; 423 C; 408 G; 339 T; 0 other;
 SQ
 Query Match 98.8%; Score 740.8; DB 13; Length 1683;
 Best Local Similarity 99.7%; Pred. No. 7.1e-148;
 Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ATGAAAAGAAATAGTCCAAAGTCTACTGAAATCTTCCCGTGGAGGACGCGAACTACCT 60
 DB 51 ATGAAAAGAAATAGTCCAAAGTCTACTGAAATCTTCCCGTGGAGGACGCGAACTACCT 110
 QY 61 TACAGCGCTTCATCGCGTCCGTCGCGGAAAGACGTGATCAACACTGACCGACCATAAA 120
 DB 111 TACAGCGCTTCATCGCGTCCGTCGCGGAAAGACGTGATCAACACTGACCGACCATAAA 170
 QY 121 GGGATCTTCCAGCCCGTGTCCACCGGAGAGAGAGTCCCGAGCTATGTTTACACA 180
 DB 171 GGGATCTTCCAGCCCGTGTCCACCGGAGAGAGAGTCCCGAGCTATGTTTACACA 230
 QY 181 GAACTGAAACTAGGACCACTGCTCAGCTCGGCATACGATCGCAACCTGTACCTC 240
 DB 231 GAGCTCAAAACTAGGACCACTGCTCAGCTCGGCATACGATCGCAACCTGTACCTC 290
 QY 241 GTGGGCTTCAGGACCCCGCGGGGTGTGTGGAGATTTCGGCAAGGACGCGGACACCCAC 300

DB 291 GTGGGCTTCAGGACCCCGCGGGGTGTGTGGAGATTTCGGCAAGGACGCGGACACCCAC 350
 QY 301 TTCTTCGGCGCAAAACCCAGGTGGCTGGCTTCGGCGGAGGTACCAAGGACCTCATCGGC 360
 DB 351 TTCTTCGGCGCAAAACCCAGGTGGCTGGCTTCGGCGGAGGTACCAAGGACCTCATCGGC 410
 QY 361 AACAGGCTCTGGAGACCGTCAACATGGCGCGCCGAAATGACAGGCGCGTCAACGAC 420
 DB 411 AACAGGCTCTGGAGACCGTCAACATGGCGCGCCGAAATGACAGGCGCGTCAACGAC 470
 QY 421 CTGGCGAAAGAGAGAGGCGGCTGACCCACAGGCGCGACAGAGAGCAAGCTGTGAAG 480
 DB 471 CTGGCGAAAGAGAGAGGCGGCTGACCCACAGGCGCGACAGAGAGCAAGCTGTGAAG 530
 QY 481 CTGGTGGTCATGGTGTGGAGGGGTGGCTTCAACACCGTGTCCGACCGTGGAGCGG 540
 DB 531 CTGGTGGTCATGGTGTGGAGGGGTGGCTTCAACACCGTGTCCGACCGTGGAGCGG 590
 QY 541 GGGTTCAACAGCAGCAGCGGGGTGACCTTGACCGTGAACGAGGGAAGCAGGTGCAGAAG 600
 DB 591 GGGTTCAACAGCAGCAGCGGGGTGACCTTGACCGTGAACGAGGGAAGCAGGTGCAGAAG 650
 QY 601 TGGGACAGGATCTCAAGGCGGCTTCGAGTGGGTGACCAACCGTGTGATCGTTCATCC 660
 DB 651 TGGGACAGGATCTCAAGGCGGCTTCGAGTGGGTGACCAACCGTGTGATCGTTCATCC 710
 QY 661 GACATCGAGAGCTTGGCATCAAGGATAAGAACGAGCAGGAGATCGTTGCGCTCGTT 720
 DB 711 GACATCGAGAGCTTGGCATCAAGGATAAGAACGAGCAGGAGATCGTTGCGCTCGTT 770
 QY 721 AAGAATCAAACTACTGCGCGTGCC 744
 DB 771 AAGAATCAAACTACTGCGCGTGCC 794
 RESULT 14
 AAT79868
 ID AAT79868 standard; DNA; 1683 BP.
 XX
 AC AAT79868;
 XX
 DT 25-MAR-2003 (updated)
 DT 01-DEC-1997 (first entry)
 XX
 XX Pro-ribosome inactivating protein gene clone RDT-G-G-A.
 XX
 KW Maize; proRIP; ribosome inactivating protein; alpha; beta subunit;
 KW internal linker; Barley Translation Inhibitor; Trichosanthin;
 KW Ricin A-chain; Abrin-A A-chain; Saporin; SLT-1; Luffin A; MAP;
 KW Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30;
 KW therapeutic toxin; tumour cell targeted; protein synthesis inhibitor;
 KW post-translational modification; cancer; neoplasia; HIV; AIDS;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; ss.
 XX
 OS Zea mays.
 XX
 FH Key Location/Qualifiers
 FT CDS 51..1520
 FT /*tag= a
 XX
 XX US5646026-A.
 PN
 XX
 PD 08-JUL-1997.
 XX
 XX 07-JUN-1995; 95US-0485286.
 PF
 XX 09-DEC-1992; 92US-0987927.
 PR 11-JUN-1990; 90US-0535636.
 PR 28-JAN-1995; 95US-0378761.
 PR 07-JUN-1995; 95US-0485286.
 XX
 PA (DOWC) DOWELANCO.

XX Hey TD, Morgan AER, Walsh TA;
 XX WPI; 1997-362934/33.
 DR P-PSDB; AAW25130.
 XX
 XX DNA encodes pro-ribosome inactivating proteins - inactive
 PT precursors of ribosome inactivating proteins; can be expressed in
 PT eukaryotic cells without causing cell death
 XX
 XX Claim 2; Column 67-72; 186pp; English.
 XX
 XX AAT79868 encodes a single chain maize pro-ribosome inactivating protein
 CC (proRIP) having a truncated leader sequence and carboxy terminus
 CC engineered for expression in *Escherichia coli* and which binds to
 CC immunoglobulin IgG. The construct has a sequence encoding the single
 CC antibody binding region (ABR) domain from *Staphylococcus aureus*
 CC antibody binding Protein A (ABR-A) and two Streptococcal Group G
 CC protein G (ABR-G) polypeptides inserted into a BamHI site. The
 CC sequence contains no linker separating the alpha and beta subunit
 CC regions and was shown to be a potent inhibitor of protein synthesis
 CC and bound specifically to IgG.
 CC proRIP sequences can be engineered to contain a selectively removable
 CC internal peptide linker sequence separating the alpha and beta units
 CC of the RIP protein to form an inactive form of RIP. When separated
 CC the two units regain activity and are capable of inactivating eukaryotic
 CC ribosomes and hence preventing protein production. Many different
 CC Panacoidae RIPs may be produced with an internal linker including:
 CC Barley translation inhibitor, Itrichosanthin, Ricin A-chain, Abrin-A
 CC A-chain, Saparin, SUT-1, Luffin A, MAP, Ricinus communis agglutinin,
 CC Momordin, PAP-S, Luffin-B and Dianthin 30. The RIPs can be used in
 CC the construction of therapeutic toxins targeted to specific cells such
 CC as tumour cells via the attachment of a targeting polypeptide, e.g. a
 CC monoclonal antibody. A further use is in HIV therapy (see US4869903).
 CC There is interest in expressing RIP recombinantly in host eukaryotic
 CC cells, because of the capacity to provide correct post-translational
 CC processing. However, RIPs effectively inhibit protein synthesis in
 CC eukaryotic cells resulting in cell death. Since the proRIP proteins
 CC are not cytotoxic to eukaryotic cells, they can be recombinantly
 CC expressed in such cells and then converted to active RIP proteins.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 XX Sequence 1683 BP; 513 A; 419 C; 412 G; 339 T; 0 other;
 SQ

Query Match 98.8%; Score 740.8; DB 18; Length 1683;
 Best Local Similarity 99.7%; Pred. No. 7.1e-148;
 Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAAGAAAGTCCAAAGTCTCACTGAATCTTCCCGTGGAGGCGGAACCTACCT 60
 DB 51 ATGAAAGAAAGTCCAAAGTCTCACTGAATCTTCCCGTGGAGGCGGAACCTACCT 110
 QY 61 TACAGGGCTTCATCGCGTCCGTCGGAAAGACGTGATCAACACCTGACCGACCAATAA 120
 DB 111 TACAGGGCTTCATCGCGTCCGTCGGAAAGACGTGATCAACACCTGACCGACCAATAA 170
 QY 121 GGGATCTTCAGCCCGTCTGCACCGAGAGAGAGTCCCGGAGCTATGTTTACACA 180
 DB 171 GGGATCTTCAGCCCGTCTGCACCGAGAGAGAGTCCCGGAGCTATGTTTACACA 230
 QY 181 GAACCTGAAACCTAGGACACGCTCCATCAGCTCGCCATACGATCGGACCACTGTACCTC 240
 DB 231 GAGCTCAAACTAGGACCAAGCTCCATCAGCTCGCCATACGATCGGACCACTGTACCTC 290
 QY 241 GTGGGCTTCAGACCCCGCGGGGTGTGTGGAGTTTCGGAAGACGGCGACACCCAC 300
 DB 291 GTGGGCTTCAGACCCCGCGGGGTGTGTGGAGTTTCGGAAGACGGCGACACCCAC 350
 QY 301 CTCCTCGGCGAACAACCCAGGTGGCTCGGCTTCGCGCGGAGTACCGAGCTCATCGGC 360
 DB 351 CTCCTCGGCGAACAACCCAGGTGGCTCGGCTTCGCGCGGAGTACCGAGCTCATCGGC 410
 QY 361 AACAGGGTCTGAGAGACCGTCCACCATGGGCGCGCGAAATGACCAGGGCGGTCAACGAC 420

DB 411 AACAGGGTCTGAGAGACCGTCCATGGGCGCGCGAAATGACAGGGCGGTCAAAGAC 470
 QY 421 CTGGCGAAAGAAAGAGAGCGGCTGACCCACAGCGCCGACAGAGAGCAAGCTGGTGAAG 480
 DB 471 CTGGCGAAAGAAAGAGAGCGGCTGACCCACAGCGCCGACAGAGAGCAAGCTGGTGAAG 530
 QY 481 CTGGTGGTCTATGGTGTGGAGGGCTGCGGTTCACACCGTGTCCGACGGTGGAGCG 540
 DB 531 CTGGTGGTCTATGGTGTGGAGGGCTGCGGTTCACACCGTGTCCGACGGTGGAGCG 590
 QY 541 GGGTTCAACAGCCAGCAGCGGGTGCCTTGCCTGACGCGAGGGGAAAGAGCTGACGAAG 600
 DB 591 GGGTTCAACAGCCAGCAGCGGGTGCCTTGCCTGACGCGAGGGGAAAGAGCTGACGAAG 650
 QY 601 TGGGACAGGATCTCAAGCGCGCTTCAGTGGGTGACACCCACCGCTGTGATCCCC 660
 DB 651 TGGGACAGGATCTCAAGCGCGCTTCAGTGGGTGACACCCACCGCTGTGATCCCC 710
 QY 661 GACATGCAAGCTTGGCATCAAGGATAAGAACGAGCAGCGAGGATCGTTGCGCTCGTT 720
 DB 711 GACATGCAAGCTTGGCATCAAGGATAAGAACGAGCAGCGAGGATCGTTGCGCTCGTT 770
 QY 721 AAGAATCAAACTACTGCGCTGCC 744
 DB 771 AAGAATCAAACTACTGCGCTGCC 794

RESULT 15
 AAT77760
 ID AAT77760 standard; DNA; 1683 BP.
 XX
 AC AAT77760;
 XX
 DT 25-MAR-2003 (updated)
 DT 26-SEP-1997 (first entry)
 XX
 DE RIP fusion protein, RDT-G-GA coding sequence.
 KW pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer;
 KW inactivator; eukaryotic ribosome; alpha fragment; beta fragment;
 KW inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver;
 KW rat; ribosomal 28S RNA; cellular proliferation; HIV-infected T cell; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT CDS 51..1520
 FT /*tag= a
 FT /product= RDT-G-GA
 XX
 PN US5635384-A.
 XX
 XX 03-JUN-1997.
 XX
 XX 26-JAN-1995; 95US-0378761.
 XX
 XX 09-DEC-1992; 92US-0987927.
 PR 11-JUN-1990; 90US-0535636.
 PR 26-JAN-1995; 95US-0378761.
 XX
 PA (DOWC) DOWELANCO.
 XX
 PI Hey TD, Morgan AER, Walsh TA;
 XX
 DR WPI; 1997-309831/28.
 DR P-PSDB; AAW21717.
 XX
 PT Inactive precursor of maize ribosome-inactivating protein - also
 PT chimeric ribosome-inactivating protein precursors containing
 XX internal linker sequences
 PS Claim 4; Column 67-70; 121pp; English.

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OM nucleic - nucleic search, using sw model

Run on: October 22, 2003, 04:23:14 ; Search time 2892 Seconds
(without alignments)
10609.343 Million cell updates/sec

Title: US-09-978-273-2

Perfect score: 750

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.on.*

5: gb.ov.*

6: gb.pat.*

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8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

17: em.hum.*

18: em.in.*

19: em.mu.*

20: em.on.*

21: em.or.*

22: em.ov.*

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34: em.htg.pln.*

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39: em.htgo.hum.*

40: em.htgo.mus.*

41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	750	100.0	750	6	AX427661	AX427661 Sequence
2	740.8	98.8	847	6	I44710	I44710 Sequence 20
3	740.8	98.8	847	6	I52116	I52116 Sequence 20
4	740.8	98.8	978	6	I44705	I44705 Sequence 10
5	740.8	98.8	978	6	I52111	I52111 Sequence 10
6	740.8	98.8	985	6	I44704	I44704 Sequence 8
7	740.8	98.8	985	6	I52110	I52110 Sequence 8
8	740.8	98.8	1161	6	I44707	I44707 Sequence 14
9	740.8	98.8	1161	6	I52113	I52113 Sequence 14
10	740.8	98.8	1422	6	I44708	I44708 Sequence 16
11	740.8	98.8	1422	6	I52114	I52114 Sequence 16
12	740.8	98.8	1683	6	I44709	I44709 Sequence 18
13	740.8	98.8	1683	6	I52115	I52115 Sequence 18
14	740.8	98.8	1695	6	I44711	I44711 Sequence 22
15	740.8	98.8	1695	6	I52117	I52117 Sequence 22
16	740.8	98.8	1722	6	I44712	I44712 Sequence 24
17	740.8	98.8	1722	6	I52118	I52118 Sequence 24
18	737.8	98.4	1029	6	I44703	I44703 Sequence 6
19	737.8	98.4	1029	6	I52109	I52109 Sequence 6
20	720.2	96.0	987	6	I44706	I44706 Sequence 12
21	720.2	96.0	987	6	I52112	I52112 Sequence 12
22	707.2	94.3	987	6	AX123360	AX123360 Sequence
23	656	87.5	909	6	AX427660	AX427660 Sequence
24	655.8	87.4	1074	6	I44702	I44702 Sequence 4
25	655.8	87.4	1074	6	I52108	I52108 Sequence 4
26	654.2	87.2	1059	6	AX123363	AX123363 Sequence
27	652.8	87.0	1076	6	I44700	I44700 Sequence 1
28	652.8	87.0	1076	6	I52106	I52106 Sequence 1
29	652.8	87.0	1076	6	MZERIP	M7122 Z.mays ribo
30	652.8	87.0	1105	6	I44701	I44701 Sequence 3
31	652.8	87.0	1105	6	I52107	I52107 Sequence 3
32	652.6	87.0	1053	6	AX123366	AX123366 Sequence
33	649.8	86.6	944	6	AX123368	AX123368 Sequence
34	649.8	86.6	1244	6	AX123372	AX123372 Sequence
35	644.2	85.9	1039	8	MZERIP3A	M83926 Zea mays ri
36	638.4	85.1	1826	8	ZMB32152	X70154 Z.mays mRNA
37	636.8	84.9	1245	6	AX123374	AX123374 Sequence
38	632.2	84.3	976	8	MZERIP9A	M83927 Zea mays ri
39	628.8	83.8	959	8	ZMA300265	AJ300265 Zea mays
40	627.4	83.7	2741	8	ZMB32129	X70153 Z.mays mRNA
41	607.6	81.0	3093	8	ZMB32120	X54212 Z.mays mRNA
42	606	80.8	1044	8	ZMALB332	X07987 Maize mRNA
43	521.4	69.5	983	8	AF233881	AF233881 Zea mays
44	510.8	68.1	963	8	MZERIP2A	L26305 Zea mays ri
45	510.8	68.1	1934	6	I25465	I25465 Sequence 1

ALIGNMENTS

RESULT 1
AX427661
LOCUS AX427661 750 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 2 from Patent WO0233106.
ACCESSION AX427661
VERSION AX427661.1 GI:21537780
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
Clade; Panicoideae; Andropogoneae; Zea.
1
REFERENCE
AUTHORS Neelam.A., Atkinson.H.J., Mcpherson.M.J. and Thomas.C.J.R.
TITLE Plant cell death system

JOURNAL Patent: WO 0233106-A 2 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)
FEATURES Location/Qualifiers
source 1..750
misc_feature 1..13
variation 181..186
misc_feature 745..750
BASE COUNT 185 a 217 c 232 g 116 t
ORIGIN

Query Match 100.0%; Score 750; DB 6; Length 750;
Best Local Similarity 100.0%; Pred. No. 1.3e-104;
Matches 750; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAAGAAATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGGACGCGAACTACCCCT 60
Db 1 ATGAAAGAAATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGGACGCGAACTACCCCT 60
QY 61 TACAGGCGCTTTCATCGCGTCCGGAAGAGCGTGAACAACTGACCGGACCGATAAA 120
Db 61 TACAGGCGCTTTCATCGCGTCCGGAAGAGCGTGAACAACTGACCGGACCGATAAA 120
QY 121 GGGATCTTCCAGCCCGTGTGCCACCGGAGAAAGTCCCGGAGTATGTTTCTACACA 180
Db 121 GGGATCTTCCAGCCCGTGTGCCACCGGAGAAAGTCCCGGAGTATGTTTCTACACA 180
QY 181 GAACTGAAACTAGGACCGAGTCCATACGCTCGCCATACGATGACAACTGTGTAACCTC 240
Db 181 GAACTGAAACTAGGACCGAGTCCATACGCTCGCCATACGATGACAACTGTGTAACCTC 240
QY 241 GTGGGCTTCAGGACCCCGGGGGTGTGGTGGAGTTCGGGAGGACCGGACCGACCCAC 300
Db 241 GTGGGCTTCAGGACCCCGGGGGTGTGGTGGAGTTCGGGAGGACCGGACCGACCCAC 300
QY 301 CTCTCGGCGCAACACCCAGGTGGCTCGGCTCGGCGGAGTACCGAGACCTCATCGGC 360
Db 301 CTCTCGGCGCAACACCCAGGTGGCTCGGCTCGGCGGAGTACCGAGACCTCATCGGC 360
QY 361 AACAGGGTCTGGAGACCGTCAACACCGTGTCCCGGACCGTGGAGGAG 420
Db 361 AACAGGGTCTGGAGACCGTCAACACCGTGTCCCGGACCGTGGAGGAG 420
QY 421 CTGGGCGAAGAAAGAGCGGCTGACCCACAGGCGGACACGAGAGGAGCTGTGAAG 480
Db 421 CTGGGCGAAGAAAGAGCGGCTGACCCACAGGCGGACACGAGAGGAGCTGTGAAG 480
QY 541 GGGTTCAACAGCAGCAGCGGGTGCCTTGAACCGTGAACCGGAGAGGAG 600
Db 541 GGGTTCAACAGCAGCAGCGGGTGCCTTGAACCGTGAACCGGAGAGGAG 600
QY 601 TGGGACAGGATCTCAAAGGCGGCTTCGAGTGGGCTGACCCACCGCTGTGATCCGC 660
Db 601 TGGGACAGGATCTCAAAGGCGGCTTCGAGTGGGCTGACCCACCGCTGTGATCCGC 660
QY 661 GACATGCAAGAGCTTGGCATCAAGGATGAAGAACGAGGAGGATCGTTGCGCTCGTT 720
Db 661 GACATGCAAGAGCTTGGCATCAAGGATGAAGAACGAGGAGGATCGTTGCGCTCGTT 720
QY 721 AAGAAATCAAACTACTGCGCGTCCCTAAATAA 750
Db 721 AAGAAATCAAACTACTGCGCGTCCCTAAATAA 750

RESULT 2
LOCUS I44710
DEFINITION Sequence 20 from patent US 5635384.
ACCESSION I44710
VERSION I44710.1 GI:2469423
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 847)
AUTHORS Walsh, T.A., Hey, T.D. and Morgan, A.B.R.
TITLE Ribosome-inactivating proteins, inactive precursor forms thereof, a process for making and a method of using
JOURNAL Patent: US 5635384-A 20 03-JUN-1997;
FEATURES Location/Qualifiers
source 1..847
BASE COUNT 212 a 240 c 254 g 141 t
ORIGIN

Query Match 98.8%; Score 740.8; DB 6; Length 847;
Best Local Similarity 99.7%; Pred. No. 3.1e-103;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAAGAAATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGGACGCGAACTACCCCT 60
Db 51 ATGAAAGAAATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGGACGCGAACTACCCCT 110
QY 61 TACAGCGCTTTCATCGCGTCCGGAAGAGCGTGAACAACTGACCGGACCGATAAA 120
Db 111 TACAGCGCTTTCATCGCGTCCGGAAGAGCGTGAACAACTGACCGGACCGATAAA 170
QY 121 GGGATCTTCCAGCCCGTGTGCCACCGGAGAAAGTTCGGGAGTATGTTTCTACACA 180
Db 171 GGGATCTTCCAGCCCGTGTGCCACCGGAGAAAGTTCGGGAGTATGTTTCTACACA 230
QY 181 GAACTGAAACTAGGACCGAGTCCATACGCTCGCCATACGATGACAACTGTGTAACCTC 240
Db 231 GAGCTCAAAACTAGGACCGAGTCCATACGCTCGCCATACGATGACAACTGTGTAACCTC 290
QY 241 GTGGGCTTCAGGACCCCGGGGGTGTGGTGGAGTTCGGGAGGACCGGACCGACCCAC 300
Db 291 GTGGGCTTCAGGACCCCGGGGGTGTGGTGGAGTTCGGGAGGACCGGACCGACCCAC 350
QY 301 CTCTCGGCGCAACACCCAGGTGGCTCGGCTCGGCGGAGTACCGAGACCTCATCGGC 360
Db 351 CTCTCGGCGCAACACCCAGGTGGCTCGGCTTCGGGCGGAGTACCGAGACCTCATCGGC 410
QY 361 AACAGGGTCTGGAGACCGTCAACATGGGCGCGCGGAAATGACAGGCGGCTGACCGAC 420
Db 411 AACAGGGTCTGGAGACCGTCAACATGGGCGCGCGGAAATGACAGGCGGCTGACCGAC 470
QY 421 CTGGGCGAAGAAAGAGCGGCTGACCCACAGGCGGACACGAGAGGAGCTGTGAAG 480
Db 471 CTGGGCGAAGAAAGAGCGGCTGACCCACAGGCGGACACGAGAGGAGCTGTGAAG 530
QY 481 CTGGTGGTTCATGGTGTGGAGGGGTGCGGTTCAACACCGTGTCCCGACCGGTGAACGG 540
Db 531 CTGGTGGTTCATGGTGTGGAGGGGTGCGGTTCAACACCGTGTCCCGACCGGTGAACGG 590
QY 541 GGGTTCAACAGCAGCAGCGGGTGCCTTGAACCGTGAACCGGAGGAGGAGCTGTGAAG 600
Db 591 GGGTTCAACAGCAGCAGCGGGTGCCTTGAACCGTGAACCGGAGGAGGAGCTGTGAAG 650
QY 601 TGGGACAGGATCTCAAAGGCGGCTTCGAGTGGGCTGACCCACCGCTGTGATCCGC 660
Db 651 TGGGACAGGATCTCAAAGGCGGCTTCGAGTGGGCTGACCCACCGCTGTGATCCGC 710
QY 661 GACATGCAAGAGCTTGGCATCAAGGATGAAGAACGAGGAGGATCGTTGCGCTCGTT 720
Db 711 GACATGCAAGAGCTTGGCATCAAGGATGAAGAACGAGGAGGATCGTTGCGCTCGTT 770

QY 721 AAGATCAAACTACTGCGCTGCC 744
 Db 771 AAGATCAAACTACTGCGCTGCC 794

RESULT 3
 152116
 LOCUS 847 bp DNA linear PAT 07-OCT-1997
 DEFINITION Sequence 20 from patent US 5646026.
 ACCESSION 152116
 VERSION 152116.1 GI:2473317
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 847)
 AUTHORS Walsh,T.A., Hey,T.D. and Morgan,A.E.R.
 TITLE Ribosome-inactivating proteins, inactive precursor forms thereof, a process for making and a method of using
 JOURNAL Patent: US 5646026-A 20 08-JUL-1997;
 FEATURES Location/Qualifiers
 source 1..847
 BASE COUNT 212 a 240 c 254 g 141 t
 ORIGIN
 Query Match 98.8%; Score 740.8; DB 6; Length 847;
 Best Local Similarity 99.7%; Pred. No. 3.1e-103;
 Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAAAGATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGACGCAACTACCT 60
 Db 51 ATGAAAAGATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGACGCAACTACCT 110
 QY 61 TACAGCGCTTCATCGCTGCTGCCGAGAGAGTGTATCAACACTGCCACCGACATAA 120
 Db 111 TACAGCGCTTCATCGCTGCTGCCGAGAGAGTGTATCAACACTGCCACCGACATAA 170
 QY 121 GGGATCTTCCAGCCGCTGCTGCCACCGAGAGAGTGTCCGGAGTGTATGTTCTACACA 180
 Db 171 GGGATCTTCCAGCCGCTGCTGCCACCGAGAGAGTGTCCGGAGTGTATGTTCTACACA 230
 QY 181 GAACTGAAAACCTAGGACCACTCCATCAGCTCCGATACGATGGACAACTGTACCTC 240
 Db 291 GTGGCTTCAGGACCCCGGGCGGGTGTGGTGGAGTTCGGCAAGGACGCGACACCCAC 350
 QY 301 CTCCTCGGCGCAACCCCGAGTGTGGTTCGGCGGAGGTACGAGACCTCATCGGC 360
 Db 351 CTCCTCGGCGCAACCCCGAGTGTGGTTCGGCGGAGGTACGAGACCTCATCGGC 410
 QY 361 AACAAAGGTCTGAGACCGTCAACATGGCGCGCCGCAATGACAGGCGCGTCAACGAC 420
 Db 471 CTGGCGAAGAGAGAGGCGGCTGACCCACAGCGCGACACGAGAGCAAGTGGTGAAG 530
 QY 481 CTGTGGTTCATGGTGTGGAGGGCTGGGTTCAACACCGTGTCCCGACGCGTGGACGG 540
 Db 531 CTGTGGTTCATGGTGTGGAGGGCTGGGTTCAACACCGTGTCCCGACGCGTGGACGG 590
 QY 541 GGGTTCAACAGCAGCAGCGGGTGCACCTTGACCGTGAACGAGGAGAGCGAGTGCAGAG 600
 Db 591 GGGTTCAACAGCAGCAGCGGGTGCACCTTGACCGTGAACGAGGAGAGCGAGTGCAGAG 650
 QY 601 TGGGACAGGATCTCAAGCGGCGCTTCAGTGGGCTGACACCCCAACCGTGTGATCCCC 660
 Db 651 TGGGACAGGATCTCAAGCGGCGCTTCAGTGGGCTGACACCCCAACCGTGTGATCCCC 710

QY 661 GACATGAGAGAGCTTGGCATCAAGGATAAGAACGAGCAGGAGATCGTTGGCTCGTT 720
 Db 711 GACATGAGAGAGCTTGGCATCAAGGATAAGAACGAGCAGGAGATCGTTGGCTCGTT 770

QY 721 AAGATCAAACTACTGCGCTGCC 744
 Db 771 AAGATCAAACTACTGCGCTGCC 794

RESULT 4
 144705
 LOCUS 978 bp DNA linear PAT 07-OCT-1997
 DEFINITION Sequence 10 from patent US 5635384.
 ACCESSION 144705
 VERSION 144705.1 GI:2459418
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 978)
 AUTHORS Walsh,T.A., Hey,T.D. and Morgan,A.E.R.
 TITLE Ribosome-inactivating proteins, inactive precursor forms thereof, a process for making and a method of using
 JOURNAL Patent: US 5635384-A 10 03-JUN-1997;
 FEATURES Location/Qualifiers
 source 1..978
 BASE COUNT 250 a 271 c 275 g 182 t
 ORIGIN
 Query Match 98.8%; Score 740.8; DB 6; Length 978;
 Best Local Similarity 99.7%; Pred. No. 3.1e-103;
 Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAAAGATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGACGCAACTACCT 60
 Db 51 ATGAAAAGATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGACGCAACTACCT 110
 QY 61 TACAGCGCTTCATCGCTGCTGCCGAGAGAGTGTATCAACACTGCCACCGACATAA 120
 Db 111 TACAGCGCTTCATCGCTGCTGCCGAGAGAGTGTATCAACACTGCCACCGACATAA 170
 QY 121 GGGATCTTCCAGCCGCTGCTGCCACCGAGAGAGTGTCCGGAGTGTATGTTCTACACA 180
 Db 171 GGGATCTTCCAGCCGCTGCTGCCACCGAGAGAGTGTCCGGAGTGTATGTTCTACACA 230
 QY 181 GAACTGAAAACCTAGGACCACTCCATCAGCTCCGATACGATGGACAACTGTACCTC 240
 Db 231 GAGCTCAAACTAGGACCACTCCATCAGCTCCGATACGATGGACAACTGTACCTC 290
 QY 241 GTGGCTTCAGGACCCCGGGCGGGTGTGGTGGAGTTCGGCAAGGACGCGGACACCCAC 300
 Db 291 GTGGCTTCAGGACCCCGGGCGGGTGTGGTGGAGTTCGGCAAGGACGCGGACACCCAC 350
 QY 301 CTCCTCGGCGCAACCCCGAGTGTGGTTCGGCGGAGGTACGAGACCTCATCGGC 360
 Db 351 CTCCTCGGCGCAACCCCGAGTGTGGTTCGGCGGAGGTACGAGACCTCATCGGC 410
 QY 361 AACAAAGGTCTGAGACCGTCAACATGGCGCGCCGCAATGACAGGCGCGTCAACGAC 420
 Db 411 AACAAAGGTCTGAGACCGTCAACATGGCGCGCCGCAATGACAGGCGCGTCAACGAC 470
 QY 421 CTGGCGAAGAGAGAGGCGGCTGACCCACAGCGCGACACGAGAGCAAGTGGTGAAG 480
 Db 471 CTGGCGAAGAGAGAGGCGGCTGACCCACAGCGCGACACGAGAGCAAGTGGTGAAG 530
 QY 481 CTGTGGTTCATGGTGTGGAGGGCTGGGTTCAACACCGTGTCCCGACGCGTGGACGG 540
 Db 531 CTGTGGTTCATGGTGTGGAGGGCTGGGTTCAACACCGTGTCCCGACGCGTGGACGG 590
 QY 541 GGGTTCAACAGCAGCAGCGGGTGCACCTTGACCGTGAACGAGGAGAGCGAGTGCAGAG 600

Db 591 GGGTTCAACAGCCAGCA CGGGGTGACCTTGACCGTGACGAGGGGAAGCAGGTGCAGAAG 650
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QY 661 GACATGCAAGAGCTTGGCATCAGGATAAGAAAGCAAGCAGGAGATCGTTGGCGTCGTT 720
Db 711 GACATGCAAGAGCTTGGCATCAGGATAAGAAAGCAAGCAGGAGATCGTTGGCGTCGTT 770
QY 721 AAGAATCAAACTACTGCGCTGCC 744
Db 771 AAGAATCAAACTACTGCGCTGCC 794

RESULT 5
152111
LOCUS 152111
DEFINITION Sequence 10 from patent US 5646026.
ACCESSION 152111
VERSION 152111.1 GI:2473312
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 978)
AUTHORS Walsh,T.A., Hey,T.D. and Morgan,A.E.R.
TITLE Ribosome-inactivating proteins, inactive precursor forms thereof, a process for making and a method of using
JOURNAL Patent: US 5646026-A 10 08-JUL-1997;
FEATURES Location/Qualifiers
source 1..978
BASE COUNT 250 a 271 c 275 g 182 t
ORIGIN

Query Match 98.8%; Score 740.8; DB 6; Length 978;
Best Local Similarity 99.7%; Pred. No. 3.1e-103;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAAGAAATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGACGCGAACTACCTT 60
Db 51 ATGAAAGAAATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGACGCGAACTACCTT 110
QY 61 TACAGCGCTTCATCGCGTCCGGAAGAGCGTGATCAAACTGCACCGACCAATAA 120
Db 111 TACAGCGCTTCATCGCGTCCGGAAGAGCGTGATCAAACTGCACCGACCAATAA 170
QY 121 GGGATCTCCAGCCGTGTGCCACCGGAGAGAGGTCCCGAGGTATGGTTCTACACA 180
Db 171 GGGATCTCCAGCCGTGTGCCACCGGAGAGAGGTCCCGAGGTATGGTTCTACACA 230
QY 181 GAACCTGAAATAGGACCACTCCATCAGCTCGCCATACGATGACAACTGTACCTC 240
Db 231 GAGCTCAAACTAGGACCACTCCATCAGCTCGCCATACGATGACAACTGTACCTC 290
QY 241 GTGGGTTTCAGACCCCGGGGGGTGTGGTGGAGTTCGGCAAGACCGGACACCCAC 300
Db 291 GTGGGTTTCAGACCCCGGGGGGTGTGGTGGAGTTCGGCAAGACCGGACACCCAC 350
QY 301 CTCCTCGGCGCAACCCCGAGGTGGCTCGGCTTTCGGGGGAGGTACGAGACCTCATCGG 360
Db 351 CTCCTCGGCGCAACCCCGAGGTGGCTCGGCTTTCGGGGGAGGTACGAGACCTCATCGG 410
QY 361 AACAGGGTCTGGAGACCGCTCAACATGGGCCCGCGGAATGACAGGCGCGTCAACGAC 420
Db 411 AACAGGGTCTGGAGACCGCTCAACATGGGCCCGCGGAATGACAGGCGCGTCAACGAC 470
QY 421 CTGGCGAAGAAAGAGCGGCTGACCAAGGCGGACACGAGGAGCAAGCTGTGGAAG 480
Db 471 CTGGCGAAGAAAGAGCGGCTGACCAAGGCGGACACGAGGAGCAAGCTGTGGAAG 530
QY 481 CTGGTGGTTCATGGTGTGGAGGGGTGCGGTTCAACACCGTGTCCCGCACGCGTGGACGG 540

Db 531 CTGGTGGTTCATGGTGTGGAGGGGCTCGGTTCAACACCGTGTCCCGCACCGTGGAGCGG 590
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QY 601 TGGGACAGGATCTCCAAAGGGCGCTTCGAGTGGGCTGACCAACCCACCGCTGTGATCCCC 660
Db 651 TGGGACAGGATCTCCAAAGGGCGCTTCGAGTGGGCTGACCAACCCACCGCTGTGATCCCC 710
QY 661 GACATCAGAGCTTGGCATCAGGATAAGAAAGCAAGCAGGAGATCGTTGGCGTCGTT 720
Db 711 GACATCAGAGCTTGGCATCAGGATAAGAAAGCAAGCAGGAGATCGTTGGCGTCGTT 770
QY 721 AAGAATCAAACTACTGCGCTGCC 744
Db 771 AAGAATCAAACTACTGCGCTGCC 794

RESULT 6
144704
LOCUS 144704
DEFINITION Sequence 8 from patent US 5635384.
ACCESSION 144704
VERSION 144704.1 GI:2469417
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 985)
AUTHORS Walsh,T.A., Hey,T.D. and Morgan,A.E.R.
TITLE Ribosome-inactivating proteins, inactive precursor forms thereof, a process for making and a method of using
JOURNAL Patent: US 5635384-A 8 03-JUN-1997;
FEATURES Location/Qualifiers
source 1..985
BASE COUNT 255 a 271 c 279 g 180 t
ORIGIN

Query Match 98.8%; Score 740.8; DB 6; Length 985;
Best Local Similarity 99.7%; Pred. No. 3.1e-103;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAAGAAATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGACGCGAACTACCTT 60
Db 37 ATGAAAGAAATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGACGCGAACTACCTT 96
QY 61 TACAGCGCTTCATCGCGTCCGGAAGAGCGTGATCAAACTGCACCGACCAATAA 120
Db 97 TACAGCGCTTCATCGCGTCCGGAAGAGCGTGATCAAACTGCACCGACCAATAA 156
QY 121 GGGATCTCCAGCCGTGTGCCACCGGAGAGAGGTCCCGAGCTATGGTTCTACACA 180
Db 157 GGGATCTCCAGCCGTGTGCCACCGGAGAGAGGTCCCGAGCTATGGTTCTACACA 216
QY 181 GAACCTGAAACTAGGACCACTCCATCAGCTCGCCATACGATGACAACTGTACCTC 240
Db 217 GAGCTCAAACTAGGACCACTCCATCAGCTCGCCATACGATGACAACTGTACCTC 276
QY 241 GTGGGCTTCAGGACCCCGGGGGGTGTGGTGGAGTTCGGCAAGACGAGCGACACCCAC 300
Db 277 GTGGGCTTCAGGACCCCGGGGGGTGTGGTGGAGTTCGGCAAGACGAGCGACACCCAC 336
QY 301 CTCCTCGGCGCAACCCCGAGGTGGCTTCGGCTTCGGCGGAGGTACGAGACCTCATCGG 360
Db 337 CTCCTCGGCGCAACCCCGAGGTGGCTTCGGCTTCGGCGGAGGTACGAGACCTCATCGG 396
QY 361 AACAGGGTCTGGAGACCGCTCACCATGGGCCCGCGGAATGACAGGCGCGTCAACGAC 420
Db 397 AACAGGGTCTGGAGACCGCTCACCATGGGCCCGCGGAATGACAGGCGCGTCAACGAC 456

QY 421 CTGGCGAAGAGAGAGCGGCTGACCCACAGCCGACACAGAGCGAAGCTGGTGAAG 480
 Db 457 CTGGCGAAGAGAGAGAGCGGCTGACCCACAGCCGACACAGAGCGAAGCTGGTGAAG 516
 QY 481 CTGGTGGTCAATGCTGCGAGGGGCTCGGCTTCAACACACCGCTGCCCGCACCGTGGACGCG 540
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 QY 601 TGGGACAGGATCTCCAAAGGCGGCTTCGAGTGGGCTGACACACCCACCGCTGTGATCCCG 660
 Db 637 TGGGACAGGATCTCCAAAGGCGGCTTCGAGTGGGCTGACACACCCACCGCTGTGATCCCG 696
 QY 661 GACATGCAAGAGCTTGGCATCAAGGATAAGAAAGCAAGCAGGAGATCGTTGGCGCTCGTT 720
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 QY 721 AAGATCAAACTACTGCGCGTGCC 744
 Db 757 AAGATCAAACTACTGCGCGTGCC 780

RESULT 7
 LOCUS I52110 985 bp DNA linear PAT 07-OCT-1997
 DEFINITION Sequence 8 from patent US 5646026.
 ACCESSION I52110
 VERSION I52110.1 GI:2473311
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 985)
 AUTHORS Walsh,T.A., Hey,T.D. and Morgan,A.E.R.
 TITLE Ribosome-inactivating proteins, inactive precursor forms thereof, a process for making and a method of using
 JOURNAL Patent: US 5646026-A 8 08-JUL-1997;
 FEATURES Location/Qualifiers
 source 1..985
 /organism="unknown"
 BASE COUNT 255 a 271 c 279 g 180 t
 ORIGIN

Query Match 98.8%; Score 740.8; DB 6; Length 985;
 Best Local Similarity 99.7%; Pred. No. 3.1e-103;
 Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAAGAGATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGGACGCGAACTACCTT 60
 Db 37 ATGAAAGAGATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGGACGCGAACTACCTT 96
 QY 61 TACAGCGCTTCATCGCGTCCGGAAGACGCTGATCAAACTCAGCAGCCACCAATAAA 120
 Db 97 TACAGCGCTTCATCGCGTCCGGAAGACGCTGATCAAACTCAGCAGCCACCAATAAA 156
 QY 121 GGGATCTTCCAGCCGCTGCTGCCACCGGAGAGAGTCCCGGAGCTATGGTTCTACACA 180
 Db 157 GGGATCTTCCAGCCGCTGCTGCCACCGGAGAGAGTCCCGGAGCTATGGTTCTACACA 216
 QY 181 GNACTGAAACTAGGACCACTCCATCAGCTCCGCATACGCATGGAACCTGTACTTC 240
 Db 217 GAGCTCAAACTAGGACCACTCCATCAGCTCCGCATACGCATGGAACCTGTACTTC 276
 QY 241 GTGGGCTTCAGGACCCCGGGGGTGTGGTGGAGTTTCGGCAAGGACGGGACACCCAC 300
 Db 277 GTGGGCTTCAGGACCCCGGGGGTGTGGTGGAGTTTCGGCAAGGACGGGACACCCAC 336
 QY 301 CTCCTCGGCGCAACCCAGGTGGCTCGGCTTCGCGCGGAGGTACGAGGACCTCATCGG 360
 Db 337 CTCCTCGGCGCAACCCAGGTGGCTCGGCTTCGCGCGGAGGTACGAGGACCTCATCGG 396

QY 361 AACAGGGTCTGGAGACCGTCAACATGGGCGCGCCGAAATGACCAGGGCGCGTCAACGAC 420
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 QY 421 CTGGCGAAGAGAGAGCGGCTGACCCACAGCCGACACAGAGAGCAAGCTGGTGAAG 480
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 QY 481 CTGGTGGTCAATGCTGCGAGGGGCTCGGCTTCAACACACCGCTGCCCGCACCGTGGACGCG 540
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 QY 601 TGGGACAGGATCTCCAAAGGCGGCTTCGAGTGGGCTGACACACCCACCGCTGTGATCCCG 660
 Db 637 TGGGACAGGATCTCCAAAGGCGGCTTCGAGTGGGCTGACACACCCACCGCTGTGATCCCG 696
 QY 661 GACATGCAAGAGCTTGGCATCAAGGATAAGAAAGCAAGCAGGAGATCGTTGGCGCTCGTT 720
 Db 697 GACATGCAAGAGCTTGGCATCAAGGATAAGAAAGCAAGCAGGAGATCGTTGGCGCTCGTT 756
 QY 721 AAGATCAAACTACTGCGCGTGCC 744
 Db 757 AAGATCAAACTACTGCGCGTGCC 780

RESULT 8
 LOCUS I44707 1161 bp DNA linear PAT 07-OCT-1997
 DEFINITION Sequence 14 from patent US 5635384.
 ACCESSION I44707
 VERSION I44707.1 GI:2469420
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1161)
 AUTHORS Walsh,T.A., Hey,T.D. and Morgan,A.E.R.
 TITLE Ribosome-inactivating proteins, inactive precursor forms thereof, a process for making and a method of using
 JOURNAL Patent: US 5635384-A 14 03-JUN-1997;
 FEATURES Location/Qualifiers
 source 1..1161
 /organism="unknown"
 BASE COUNT 327 a 309 c 302 g 223 t
 ORIGIN

Query Match 98.8%; Score 740.8; DB 6; Length 1161;
 Best Local Similarity 99.7%; Pred. No. 3e-103;
 Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAAGAGATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGGACGCGAACTACCTT 60
 Db 51 ATGAAAGAGATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGGACGCGAACTACCTT 110
 QY 61 TACAGCGCTTCATCGCGTCCGGAAGACGCTGATCAAACTCAGCAGCCACCAATAAA 120
 Db 111 TACAGCGCTTCATCGCGTCCGGAAGACGCTGATCAAACTCAGCAGCCACCAATAAA 170
 QY 121 GGGATCTTCCAGCCGCTGCTGCCACCGGAGAGAGTCCCGGAGCTATGGTTCTACACA 180
 Db 171 GGGATCTTCCAGCCGCTGCTGCCACCGGAGAGAGTCCCGGAGCTATGGTTCTACACA 230
 QY 181 GNACTGAAACTAGGACCACTCCATCAGCTCCGCATACGCATGGAACCTGTACTTC 240
 Db 231 GAGCTCAAACTAGGACCACTCCATCAGCTCCGCATACGCATGGAACCTGTACTTC 290
 QY 241 GTGGGCTTCAGGACCCCGGGGGTGTGGTGGAGTTTCGGCAAGGACGGGACACCCAC 300

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Db      291 GTGGGCTTCAGGACCCCGGGGGTGTGGTGGAGTTCCGCAAGACGCGGACACCCAC 350
Qy      301 CTCTCCGGCGACACACCCAGGTGGCTCGGCTTCGGCGGCGAGGTACCGAGGACCTCATCGGC 360
Db      351 CTCTCCGGCGACACACCCAGGTGGCTCGGCTTCGGCGGCGAGGTACCGAGGACCTCATCGGC 410
Qy      361 AACAGGGTCTGGAGACCGTCAACATGGCGCGCGCGAATGACCAAGGCGCGTCAACGAC 420
Db      411 AACAGGGTCTGGAGACCGTCAACATGGCGCGCGCGAATGACCAAGGCGCGTCAACGAC 470
Qy      421 CTGGCGAAGAAAGAGAGGGCGGTGACCCAGCGCGGCGGACGAGAGAGAGAGAGAGAGAG 480
Db      471 CTGGCGAAGAAAGAGAGGGCGGTGACCCAGCGCGGCGGACGAGAGAGAGAGAGAGAGAG 530
Qy      481 CTGTGTGTATGTGTGGAGGGGCTCGGGTTCAACCGTGTCCCGCAGCGGTGGAGCGG 540
Db      531 CTGTGTGTATGTGTGGAGGGGCTCGGGTTCAACCGTGTCCCGCAGCGGTGGAGCGG 590
Qy      541 GGGTTCAACAGCAGCAGCGGGTCACTTGACCGTGAACGAGGAGAGAGAGAGAGAGAGAG 600
Db      591 GGGTTCAACAGCAGCAGCGGGTCACTTGACCGTGAACGAGGAGAGAGAGAGAGAGAGAG 650
Qy      601 TGGGACAGGATCTCCAGGCGGCGCTTCGAGTGGGCTGACACCCGCTGTGATCCCC 660
Db      651 TGGGACAGGATCTCCAGGCGGCGCTTCGAGTGGGCTGACACCCGCTGTGATCCCC 710
Qy      661 GACATGCAGAGCTTGGCATCAAGGATAAGAAACGAGGAGGATCGTTGCGCTCGTT 720
Db      711 GACATGCAGAGCTTGGCATCAAGGATAAGAAACGAGGAGGATCGTTGCGCTCGTT 770
Qy      721 AAGAACTCAAACTACTGCGCGTGC 744
Db      771 AAGAACTCAAACTACTGCGCGTGC 794

RESULT 9
LOCUS      152113
DEFINITION Sequence 14 from patent US 5646026.
ACCESSION 152113
VERSION    152113.1 GI:2473314
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 1161)
AUTHORS    Walsh,T.A., Hey,T.D. and Morgan,A.E.R.
TITLE       Ribosome-inactivating proteins, inactive precursor forms thereof, a
            process for making and a method of using
JOURNAL     Patent: US 5646026-A 14 08-JUL-1997;
FEATURES    Location/Qualifiers
            source
BASE COUNT 327 a 309 c 302 g 223 t
ORIGIN

Query Match 98.8%; Score 740.8; DB 6; Length 1161;
Best Local Similarity 99.7%; Pred. No. 3e-103;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 ATGAAAGAAATAGTCCAAAGTTCACTGAAATCTTCCCGTGGAGGACGGCACTACCT 60
Db      51 ATGAAAGAAATAGTCCAAAGTTCACTGAAATCTTCCCGTGGAGGACGGCACTACCT 110
Qy      61 TACAGGCGCTTCATCGCGTGGTCCGAAAGACGAGTCAAAACACTGACCGACCATATAA 120
Db      111 TACAGGCGCTTCATCGCGTGGTCCGAAAGACGAGTCAAAACACTGACCGACCATATAA 170
Qy      121 GGGATCTCCAGCCGCTGTCGCCAGAGAGAGGTCGCGGAGCTATGTTCTACACA 180
Db      171 GGGATCTCCAGCCGCTGTCGCCAGAGAGAGGTCGCGGAGCTATGTTCTACACA 230
Qy      181 GAACTGAAAACTAGGACCACTCCATCAGCTCGCCATACGATGGACAACTGTACCTC 240

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Db      231 GAGCTCAAAATAGAGACCAAGCTCCATCAGCTCCGCTACGATAGCAACCTGTACTCTC 290
Qy      241 GTGGGCTTCAGGACCCCGGGGGTGTGGTGGAGTTCCGCAAGAGGACGCGACACCCAC 300
Db      291 GTGGGCTTCAGGACCCCGGGGGTGTGGTGGAGTTCCGCAAGAGGACGCGACACCCAC 350
Qy      301 CTCCTCGGCGACACACCCAGGTGGCTCGGCTTCGGCGGCGAGGTACCGAGGACCTCATCGGC 360
Db      351 CTCCTCGGCGACACACCCAGGTGGCTCGGCTTCGGCGGCGAGGTACCGAGGACCTCATCGGC 410
Qy      361 AACAGGGTCTGGAGACCGTCAACATGGCGCGCGCGAATGACCAAGGCGCGTCAACGAC 420
Db      411 AACAGGGTCTGGAGACCGTCAACATGGCGCGCGCGAATGACCAAGGCGCGTCAACGAC 470
Qy      421 CTGGCGAAGAAAGAGAGGGCGGTGACCCAGCGCGGCGGACGAGAGAGAGAGAGAGAGAG 480
Db      471 CTGGCGAAGAAAGAGAGGGCGGTGACCCAGCGCGGCGGACGAGAGAGAGAGAGAGAGAG 530
Qy      481 CTGGTGTGTATGTGTGGAGGGGCTCGGGTTCAACCGTGTCCCGCAGCGGTGGAGCGG 540
Db      531 CTGGTGTGTATGTGTGGAGGGGCTCGGGTTCAACCGTGTCCCGCAGCGGTGGAGCGG 590
Qy      541 GGGTTCAACAGCAGCAGCGGGTCACTTGACCGTGAACGAGGAGAGAGAGAGAGAGAGAG 600
Db      591 GGGTTCAACAGCAGCAGCGGGTCACTTGACCGTGAACGAGGAGAGAGAGAGAGAGAGAG 650
Qy      601 TGGGACAGGATCTCCAGGCGGCGCTTCGAGTGGGCTGACACCCGCTGTGATCCCC 660
Db      651 TGGGACAGGATCTCCAGGCGGCGCTTCGAGTGGGCTGACACCCGCTGTGATCCCC 710
Qy      661 GACATGCAGAGCTTGGCATCAAGGATAAGAAACGAGGAGGATCGTTGCGCTCGTT 720
Db      711 GACATGCAGAGCTTGGCATCAAGGATAAGAAACGAGGAGGATCGTTGCGCTCGTT 770
Qy      721 AAGAACTCAAACTACTGCGCGTGC 744
Db      771 AAGAACTCAAACTACTGCGCGTGC 794

RESULT 10
LOCUS      144708
DEFINITION Sequence 16 from patent US 5635384.
ACCESSION 144708
VERSION    144708.1 GI:2469421
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 1422)
AUTHORS    Walsh,T.A., Hey,T.D. and Morgan,A.E.R.
TITLE       Ribosome-inactivating proteins, inactive precursor forms thereof, a
            process for making and a method of using
JOURNAL     Patent: US 5635384-A 16 03-JUN-1997;
FEATURES    Location/Qualifiers
            source
BASE COUNT 420 a 364 c 357 g 281 t
ORIGIN

Query Match 98.8%; Score 740.8; DB 6; Length 1422;
Best Local Similarity 99.7%; Pred. No. 2.9e-103;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 ATGAAAGAAATAGTCCAAAGTTCACTGAAATCTTCCCGTGGAGGACGGCACTACCT 60
Db      51 ATGAAAGAAATAGTCCAAAGTTCACTGAAATCTTCCCGTGGAGGACGGCACTACCT 110
Qy      61 TACAGGCGCTTCATCGCGTGGTCCGAAAGACGAGTCAAAACACTGACCGACCATATAA 120
Db      111 TACAGGCGCTTCATCGCGTGGTCCGAAAGACGAGTCAAAACACTGACCGACCATATAA 170

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QY 121 GGGATCTTCCAGCCCGGTGCTGCGAAGAGAGAGTCCCGAGCTATGGTTCTACACA 180
Db 171 GGGATCTTCCAGCCCGGTGCTGCGAAGAGAGAGTCCCGAGCTATGGTTCTACACA 230
QY 181 GAACTGAAACTAGGACCACTCCATCAGCTCGCCATAGCATGGAACCTGTACCTC 240
Db 231 GAGCTCAAACTAGGACCACTCCATCAGCTCGCCATAGCATGGAACCTGTACCTC 290
QY 241 GTGGGCTTCCAGACCCCGGGGTGTGGTGGAGTTCCGCAAGAGACGGCGCACCCAC 300
Db 291 GTGGGCTTCCAGACCCCGGGGTGTGGTGGAGTTCCGCAAGAGACGGCGCACCCAC 350
QY 301 CTCTCGGCGACAAACCCAGGTGCTCGGCTTCCGCGCGAGGTACAGACCTCATCGGC 360
Db 351 CTCTCGGCGACAAACCCAGGTGCTCGGCTTCCGCGCGAGGTACAGACCTCATCGGC 410
QY 361 AACAAAGGTCTGGAGACCGTCAACATGGCGCGCGGAGTCCGCAAGAGACGGCGCACCGAC 420
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QY 421 CTGGCGAAGAGAAAGGCGGTGACCCACAGCGCCGACACAGAGCAAGCAAGCTGGTGAAG 480
Db 471 CTGGCGAAGAGAAAGGCGGTGACCCACAGCGCCGACACAGAGCAAGCAAGCTGGTGAAG 530
QY 481 CTGGTGTCTATGTGTGCGAGGGGCTCGGCTTCAACACCGTGTCCCGCACGGTGGACGG 540
Db 531 CTGGTGTCTATGTGTGCGAGGGGCTCGGCTTCAACACCGTGTCCCGCACGGTGGACGG 590
QY 541 GGGTTCAACAGCCAGACACGGGTGACCTTCAACCGTGTACGCGAGGAGCAAGCTGGTGAAG 600
Db 591 GGGTTCAACAGCCAGACACGGGTGACCTTCAACCGTGTACGCGAGGAGCAAGCTGGTGAAG 650
QY 601 TGGGACAGGATCTCCAAAGCGCGCTTCAAGTGGGCTGACCAACCGCGCTGTGATCCCC 660
Db 651 TGGGACAGGATCTCCAAAGCGCGCTTCAAGTGGGCTGACCAACCGCGCTGTGATCCCC 710
QY 661 GACATCGAGAGCTTGGCATCAGGATAAGAAACGAGAGCAAGCAAGCTGGTGGCTCGTT 720
Db 711 GACATCGAGAGCTTGGCATCAGGATAAGAAACGAGAGCAAGCAAGCTGGTGGCTCGTT 770
QY 721 AAGAATCAAACTACTGCGCGTGC 744
Db 771 AAGAATCAAACTACTGCGCGTGC 794

RESULT 11
LOCUS 152114
DEFINITION Sequence 16 from patent US 5646026.
ACCESSION 152114
VERSION 152114.1 GI:2473315
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1422)
AUTHORS Walsh,T.A., Hey,T.D. and Morgan,A.B.R.
TITLE Ribosome-inactivating proteins, inactive precursor forms thereof, a process for making and a method of using
JOURNAL Patent: US 5646026-A 16 08-JUL-1997;
FEATURES Location/Qualifiers
source 1..1422
BASE COUNT 420 a 364 c 357 g 281 t
ORIGIN
Query Match 98.8%; Score 740.8; DB 6; Length 1422;
Best Local Similarity 99.7%; Pred. No. 2.9e-103;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAAGAAATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGACGCGAATACCT 60
Db 51 ATGAAAGAAATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGACGCGAATACCT 110
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QY 61 TACAGCGCTTCACTCGCTGGTCCGGAAGAGAGTGTATCAAACTGCACCGCATATAA 120
Db 111 TACAGCGCTTCACTCGCTGGTCCGGAAGAGAGTGTATCAAACTGCACCGCATATAA 170
QY 121 GGGATCTTCCAGCCCGGTGCTGCGAAGAGAGTCCCGAGCTATGGTTCTACACA 180
Db 171 GGGATCTTCCAGCCCGGTGCTGCGAAGAGAGTCCCGAGCTATGGTTCTACACA 230
QY 181 GAACTGAAACTAGGACCACTCCATCAGCTCGCCATAGCATGGAACCTGTACCTC 240
Db 231 GAGCTCAAACTAGGACCACTCCATCAGCTCGCCATAGCATGGAACCTGTACCTC 290
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Db 291 GTGGGCTTCCAGACCCCGGGGTGTGGTGGAGTTCCGCAAGAGACGGCGCACCCAC 350
QY 301 CTCTCGGCGACAAACCCAGGTGCTCGGCTTCCGCGCGAGGTACAGACCTCATCGGC 360
Db 351 CTCTCGGCGACAAACCCAGGTGCTCGGCTTCCGCGCGAGGTACAGACCTCATCGGC 410
QY 361 AACAAAGGTCTGGAGACCGTCAACATGGCGCGCGGAGTCCGCAAGAGACGGCGCACCGAC 420
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QY 421 CTGGCGAAGAGAAAGGCGGTGACCCACAGCGCCGACACAGAGCAAGCAAGCTGGTGAAG 480
Db 471 CTGGCGAAGAGAAAGGCGGTGACCCACAGCGCCGACACAGAGCAAGCAAGCTGGTGAAG 530
QY 481 CTGGTGTCTATGTGTGCGAGGGGCTCGGCTTCAACACCGTGTCCCGCACGGTGGACGG 540
Db 531 CTGGTGTCTATGTGTGCGAGGGGCTCGGCTTCAACACCGTGTCCCGCACGGTGGACGG 590
QY 541 GGGTTCAACAGCCAGACACGGGTGACCTTCAACCGTGTACGCGAGGAGCAAGCTGGTGAAG 600
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Db 651 TGGGACAGGATCTCCAAAGCGCGCTTCAAGTGGGCTGACCAACCGCGCTGTGATCCCC 710
QY 661 GACATCGAGAGCTTGGCATCAGGATAAGAAACGAGAGCAAGCAAGCTGGTGGCTCGTT 720
Db 711 GACATCGAGAGCTTGGCATCAGGATAAGAAACGAGAGCAAGCAAGCTGGTGGCTCGTT 770
QY 721 AAGAATCAAACTACTGCGCGTGC 744
Db 771 AAGAATCAAACTACTGCGCGTGC 794

RESULT 12
LOCUS 144709
DEFINITION Sequence 18 from patent US 5635384.
ACCESSION 144709
VERSION 144709.1 GI:2469422
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1683)
AUTHORS Walsh,T.A., Hey,T.D. and Morgan,A.B.R.
TITLE Ribosome-inactivating proteins, inactive precursor forms thereof, a process for making and a method of using
JOURNAL Patent: US 5635384-A 18 03-JUN-1997;
FEATURES Location/Qualifiers
source 1..1683
BASE COUNT 513 a 419 c 412 g 339 t
ORIGIN
Query Match 98.8%; Score 740.8; DB 6; Length 1683;
Best Local Similarity 99.7%; Pred. No. 2.8e-103;
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Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		BASE COUNT 513 a 419 c 412 g 339 t	
QY	1 ATGAAAGAAATAGTGCCTGAAAGTTCACTGAAATCTTCCCGTGGAGGACGCGAACTACCCCT 60	Query Match 98.8%; Score 740.8; DB 6; Length 1683;	
Db	51 ATGAAAGAAATAGTGCCTGAAAGTTCACTGAAATCTTCCCGTGGAGGACGCGAACTACCCCT 110	Best Local Similarity 99.7%; Pred. No. 2.8e-103;	
QY	61 TACAGCGCTTCATCGCGTTCGCGGAAAGCGTATCAAACTGCAACGACGCGACCATAA 120	Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Db	111 TACAGCGCTTCATCGCGTTCGCGGAAAGCGTATCAAACTGCAACGACGCGACCATAA 170		
QY	121 GGGATCTTCAGCCGCTGCTGCCACCGGAGAAAGGTCCTGGAGCTATGGTTCTACACA 180		
Db	171 GGGATCTTCAGCCGCTGCTGCCACCGGAGAAAGGTCCTGGAGCTATGGTTCTACACA 230		
QY	181 GAACTGAAACTAGGACCACTGCTCCATCAGCTTCGCCATACGATGCAACCTGTACCTC 240		
Db	231 GAGCTCAAACTAGGACCACTGCTCCATCAGCTTCGCCATACGATGCAACCTGTACCTC 290		
QY	241 GTGGGCTTCAGACCCCGCGGGGTGTGGTGGAGTTCGGCAAGAACGCGACACCCAC 300		
Db	291 GTGGGCTTCAGACCCCGCGGGGTGTGGTGGAGTTCGGCAAGAACGCGACACCCAC 350		
QY	301 CTCCTCGGCGCAACCCAGGTGGCTCGCTTCGGCGGAGGTACAGGACCTCATCGGC 360		
Db	351 CTCCTCGGCGCAACCCAGGTGGCTCGCTTCGGCGGAGGTACAGGACCTCATCGGC 410		
QY	361 AACAAAGGTCTGGAGACCGTCACTATGGCGCGCGGAAATGACAGGGCCGTCAACGAC 420		
Db	411 AACAAAGGTCTGGAGACCGTCACTATGGCGCGCGGAAATGACAGGGCCGTCAACGAC 470		
QY	421 CTGGCGAAGAAAGAACGCGGTGACCCACAGGCGCGACACGAGAGCAAGTGTGTGAAG 480		
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QY	481 CTGGTGTCTATGGTGTGAGAGGGCTGCGGTTCAACCGTGTCCCGACGCTGGACGCG 540		
Db	531 CTGGTGTCTATGGTGTGAGAGGGCTGCGGTTCAACCGTGTCCCGACGCTGGACGCG 590		
QY	541 GGGTTCAACAGCAGCAGCGGGGTGACCTTGACCGTGCAGCGGGAAGCAGGTGCAGAA 600		
Db	591 GGGTTCAACAGCAGCAGCGGGGTGACCTTGACCGTGCAGCGGGAAGCAGGTGCAGAA 650		
QY	601 TGGGACAGATCTCAAGCGCGCTTCGAGTGGGCTGACACCCACCGCTGTGATCCCC 660		
Db	651 TGGGACAGATCTCAAGCGCGCTTCGAGTGGGCTGACACCCACCGCTGTGATCCCC 710		
QY	661 GACATGCAAGCTTGGCATCAAGGATAAGAACGAGCAGGAGTCTGCGCTCGTT 720		
Db	711 GACATGCAAGCTTGGCATCAAGGATAAGAACGAGCAGGAGTCTGCGCTCGTT 770		

RESULT 13
I52115
LOCUS
DEFINITION
Sequence 18 from patent US 5646026.
I52115
VERSION
I52115.1 GI:2473316
KEYWORDS
SOURCE
Unknown.
ORGANISM
Unknown.
Unclassified.
1 (bases 1 to 1683)
Walsh,T.A., Hey,T.D. and Morgan,A.E.R.
Ribosome-inactivating proteins, inactive precursor forms thereof, a process for making and a method of using
Patent: US 5646026-A 18 08-JUL-1997;
Location/Qualifiers
1. .1683
/organism="unknown"

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

RESULT 14
I44711
LOCUS
DEFINITION
Sequence 22 from patent US 5635384.
I44711
ACCESSION
I44711.1 GI:2469424
KEYWORDS
SOURCE
Unknown.
ORGANISM
Unknown.
Unclassified.
1 (bases 1 to 1695)
Walsh,T.A., Hey,T.D. and Morgan,A.E.R.
Ribosome-inactivating proteins, inactive precursor forms thereof, a

BASE COUNT 513 a 419 c 412 g 339 t		BASE COUNT 513 a 419 c 412 g 339 t	
QY	1 ATGAAAGAAATAGTGCCTGAAAGTTCACTGAAATCTTCCCGTGGAGGACGCGAACTACCCCT 60	Query Match 98.8%; Score 740.8; DB 6; Length 1683;	
Db	51 ATGAAAGAAATAGTGCCTGAAAGTTCACTGAAATCTTCCCGTGGAGGACGCGAACTACCCCT 110	Best Local Similarity 99.7%; Pred. No. 2.8e-103;	
QY	61 TACAGCGCTTCATCGCGTTCGCGGAAAGCGTATCAAACTGCAACGACGCGACCATAA 120	Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Db	111 TACAGCGCTTCATCGCGTTCGCGGAAAGCGTATCAAACTGCAACGACGCGACCATAA 170		
QY	121 GGGATCTTCAGCCGCTGCTGCCACCGGAGAAAGGTCCTGGAGCTATGGTTCTACACA 180		
Db	171 GGGATCTTCAGCCGCTGCTGCCACCGGAGAAAGGTCCTGGAGCTATGGTTCTACACA 230		
QY	181 GAACTGAAAACTAGGACCACTGCTCCATCAGCTTCGCCATACGATGCAACCTGTACCTC 240		
Db	231 GAGCTCAAACTAGGACCACTGCTCCATCAGCTTCGCCATACGATGCAACCTGTACCTC 290		
QY	241 GTGGGCTTCAGAACCCCGCGGGGTGTGGTGGAGTTCGGCAAGAACGCGACACCCAC 300		
Db	291 GTGGGCTTCAGAACCCCGCGGGGTGTGGTGGAGTTCGGCAAGAACGCGACACCCAC 350		
QY	301 CTCCTCGGCGCAACCCAGGTGGCTCGCTTCGGCGGAGGTACAGGACCTCATCGGC 360		
Db	351 CTCCTCGGCGCAACCCAGGTGGCTCGCTTCGGCGGAGGTACAGGACCTCATCGGC 410		
QY	361 AACAAAGGTCTGGAGACCGTCACTATGGCGCGCGGAAATGACAGGGCCGTCAACGAC 420		
Db	411 AACAAAGGTCTGGAGACCGTCACTATGGCGCGCGGAAATGACAGGGCCGTCAACGAC 470		
QY	421 CTGGCGAAGAAAGAACGCGGTGACCCACAGGCGCGACACGAGAGCAAGTGTGTGAAG 480		
Db	471 CTGGCGAAGAAAGAACGCGGTGACCCACAGGCGCGACACGAGAGCAAGTGTGTGAAG 530		
QY	481 CTGGTGTCTATGGTGTGAGAGGGCTGCGGTTCAACCGTGTCCCGACGCTGGACGCG 540		
Db	531 CTGGTGTCTATGGTGTGAGAGGGCTGCGGTTCAACCGTGTCCCGACGCTGGACGCG 590		
QY	541 GGGTTCAACAGCAGCAGCGGGGTGACCTTGACCGTGCAGCGGGAAGCAGGTGCAGAA 600		
Db	591 GGGTTCAACAGCAGCAGCGGGGTGACCTTGACCGTGCAGCGGGAAGCAGGTGCAGAA 650		
QY	601 TGGGACAGATCTCAAGCGCGCTTCGAGTGGGCTGACACCCACCGCTGTGATCCCC 660		
Db	651 TGGGACAGATCTCAAGCGCGCTTCGAGTGGGCTGACACCCACCGCTGTGATCCCC 710		
QY	661 GACATGCAAGCTTGGCATCAAGGATAAGAACGAGCAGGAGTCTGCGCTCGTT 720		
Db	711 GACATGCAAGCTTGGCATCAAGGATAAGAACGAGCAGGAGTCTGCGCTCGTT 770		

RESULT 14
I44711
LOCUS
DEFINITION
Sequence 22 from patent US 5635384.
I44711
ACCESSION
I44711.1 GI:2469424
KEYWORDS
SOURCE
Unknown.
ORGANISM
Unknown.
Unclassified.
1 (bases 1 to 1695)
Walsh,T.A., Hey,T.D. and Morgan,A.E.R.
Ribosome-inactivating proteins, inactive precursor forms thereof, a

JOURNAL		process for making and a method of using	
FEATURES		Patent: US 5635384-A 22 03-JUN-1997;	
source		Location/Qualifiers	
BASE COUNT		1..1695	
ORIGIN		/organism="unknown"	
Query Match		516 a 422 c 415 g 342 t	
Best Local Similarity		98.8%; Score 740.8; DB 6; Length 1695;	
Matches 742;		Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	1	ATGAAAGAATAGTGC	AAAGTTCACTGAAATCTTCCCGTGGAGAGCGGAACCTACCCCT 60
Db	51	ATGAAAGAATAGTGC	AAAGTTCACTGAAATCTTCCCGTGGAGAGCGGAACCTACCCCT 110
QY	61	TACAGCGCTTCATCG	CGTCCGGAAGACGTGATCAAACTGCAACGACGACCAATAA 120
Db	111	TACAGCGCTTCATCG	CGTCCGGAAGACGTGATCAAACTGCAACGACGACCAATAA 170
QY	121	GGGATCTTCCAGCCG	TGCTGCCACCGGAGAAAGTCCCGAGCTATGTTCTACACA 180
Db	171	GGGATCTTCCAGCCG	TGCTGCCACCGGAGAAAGTCCCGAGCTATGTTCTACACA 230
QY	181	GAACTGAAACTAGGAC	CAAGTCCATCAAGCTCGCCATACGATGGAACCTGCTACCTC 240
Db	231	GAGCTCAAAACTAGGAC	CAAGTCCATCAAGCTCGCCATACGATGGAACCTGCTACCTC 290
QY	301	CTCCTCGGCGCAAC	CCCCCAGGTGGCTTCGGCGGCGAGGTACCCAGACCTCATCGGC 360
Db	351	CTCCTCGGCGCAAC	CCCCCAGGTGGCTTCGGCGGCGAGGTACCCAGACCTCATCGGC 410
QY	361	AACAGGGTCTGGAG	ACCGTCAACATGGCCCGCGCGGAATGACAGGCGCGTCAACGAC 420
Db	411	AACAGGGTCTGGAG	ACCGTCAACATGGCCCGCGCGGAATGACAGGCGCGTCAACGAC 470
QY	421	CTGGCGAAGAAGAAG	AGCGCGCTGACCCACAGGCGGACACGAAAGCAAGTGTGAAG 480
Db	471	CTGGCGAAGAAGAAG	AGCGCGCTGACCCACAGGCGGACACGAAAGCAAGTGTGAAG 530
QY	481	CTGGTGGTCAATG	TGTGCGAGGGGTGCGGTTCAACACCGTGTCCCGCAGGTGACGCG 540
Db	531	CTGGTGGTCAATG	TGTGCGAGGGGTGCGGTTCAACACCGTGTCCCGCAGGTGACGCG 590
QY	541	GGGTTCAACAGCAG	CACCGGGTGACCTTGACCGTGAACGAGGGAAGCAGGTGCAGAG 600
Db	591	GGGTTCAACAGCAG	CACCGGGTGACCTTGACCGTGAACGAGGGAAGCAGGTGCAGAG 650
QY	601	TGGGACAGGATCT	CAAGCGCGCTTCCAGTGGGCTGACCCACCGCTGTGATCCCC 660
Db	651	TGGGACAGGATCT	CAAGCGCGCTTCCAGTGGGCTGACCCACCGCTGTGATCCCC 710
QY	661	GACATGCAGAAGCT	TGGCATCAAGGATAGAACGAGCAGGAGGATCGTTCGCTCGTT 720
Db	711	GACATGCAGAAGCT	TGGCATCAAGGATAGAACGAGCAGGAGGATCGTTCGCTCGTT 770
QY	721	AAGAATCAAACTAC	TGCCGCTGCC 744
Db	771	AAGAATCAAACTAC	TGCCGCTGCC 794
Search completed: October 22, 2003, 06:15:40			
Job time : 2895 secs			